

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 27, 2003, 10:53:59 ; Search time 36 Seconds
(without alignments)
359.036 Million cell updates/sec

Title: US-09-828-607-6

Perfect score: 157
Sequence: [1 XX 97]

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.GeneSeq_101002.*
1: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1980.DAT:*
2: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT:*
3: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1982.DAT:*
4: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1983.DAT:*
5: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1984.DAT:*
6: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1985.DAT:*
7: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1986.DAT:*
8: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1987.DAT:*
9: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1988.DAT:*
10: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1989.DAT:*
11: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1990.DAT:*
12: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1991.DAT:*
13: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1992.DAT:*
14: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1993.DAT:*
15: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1994.DAT:*
16: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1995.DAT:*
17: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1996.DAT:*
18: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1997.DAT:*
19: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1998.DAT:*
20: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA1999.DAT:*
21: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT:*
22: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:*
23: /SID22/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	17.8	178	20	AAV39218
2	28	17.8	178	20	AAV39075
3	27	17.2	45	22	AAO10118
4	27	17.2	58	21	AB24438
5	27	17.2	125	22	ABG05086
6	27	17.2	274	22	AAU19418
7	27	17.2	468	21	AA824499
8	26	16.6	59	22	AB839643
9	26	16.6	59	22	AB824324
10	26	16.6	59	22	AA60355

11	26	16.6	59	22	AAW72991	Human bone marrow
12	26	16.6	59	22	AAW19796	Peptide #6230 enco
13	26	16.6	59	22	AAW33215	Peptide #7252 enco
14	26	16.6	59	23	ABG42830	Human peptide enco
15	26	16.6	66	18	AAW30345	Fragment of bone m
16	26	16.6	67	23	ABP32107	Human ORF1080 prot
17	26	16.6	69	23	ABW07196	Human Ztgibeta-10
18	26	16.6	73	23	ABW07197	Human Ztgibeta-10
19	26	16.6	76	23	ABW07200	Human Ztgibeta-10
20	26	16.6	84	23	ABP51629	Human TGF-beta-R a
21	26	16.6	91	23	ABP32539	Human ORF1512 prot
22	26	16.6	98	12	AAW11947	Truncated TGF-beta
23	26	16.6	103	10	AAW1247	Protein CBMP-3. M
24	26	16.6	103	10	AAW95685	CBMP-3 protein for
25	26	16.6	103	15	AAW47294	BMP3. Homo sapien
26	26	16.6	103	20	AAW16711	WO914235 Seq ID N
27	26	16.6	103	21	AAW09529	Human BMP-3, SRO I
28	26	16.6	103	21	AAW02795	Human BMP3 amino a
29	26	16.6	103	21	AAW92564	BMP 3 finger-1-hee
30	26	16.6	103	23	ABW07204	Human BMP3(fx) sev
31	26	16.6	104	14	AAW33414	Morphogen BMP3. H
32	26	16.6	104	14	AAW33936	Human BMP3 (fx) mo
33	26	16.6	104	15	AAW46746	Human BMP3(fx) H
34	26	16.6	104	15	AAW57982	Human BMP3(fx) H
35	26	16.6	104	15	AAW50209	Human BMP3(fx) H
36	26	16.6	104	15	AAW60977	Human BMP3(fx) H
37	26	16.6	104	15	AAW60963	Human BMP3(fx) H
38	26	16.6	104	17	AAW00233	Human BMP3(fx) mor
39	26	16.6	104	17	AAW40196	Human partial BMP-
40	26	16.6	104	18	AAW36865	Conserved 7 cystel
41	26	16.6	104	19	AAW46924	Human bone morphog
42	26	16.6	104	21	AAW57234	Human bone morphog
43	26	16.6	109	14	AAW44755	Partial sequence o
44	26	16.6	109	15	AAW51642	Partial mature hum
45	26	16.6	109	17	AAW85763	Partial human CBMP

ALIGNMENTS

RESULT 1	AAV39218	AAV39218 standard; Protein: 178 AA.
XX	XX	XX
AC	AAV39218;	
XX	XX	XX
DT	05-NOV-1999 (first entry)	
XX	XX	XX
DE	M. tuberculosis antigen MO-39 amino acid sequence.	
XX	XX	XX
KW	Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;	
KM	immunotherapy; diagnosis; immunisation; vaccine; infection;	
KW	immune response; skin test.	
XX	XX	XX
OS	Mycobacterium tuberculosis.	
XX	XX	XX
PN	WO942076-A2.	
XX	XX	XX
PD	26-AUG-1999.	
XX	XX	XX
PF	17-FEB-1999; 99MO-US03268.	
XX	XX	XX
PR	05-MAY-1998; 98US-0072967.	
XX	XX	XX
PR	18-FEB-1998; 98US-0025197.	
XX	XX	XX
PA	(CORI-) CORIXA CORP.	
XX	XX	XX
PI	Campos-Melo A, Dillon DC, Hendrickson RC, Houghton R;	
XX	XX	XX
PI	Iodes KW, Reed SG, Skelky YAW, Twardzik DR, Vedvick TS;	
XX	XX	XX
DR	WPI; 1999-527409/44.	
XX	XX	XX
DR	N-PSDB; AA219414.	

Good date

PT New antigens from Mycobacterium tuberculosis useful in diagnostic
 XX skin tests and protective or therapeutic vaccines or compositions
 XX
 PS Example 5; Page 246; 299pp; English.
 XX
 CC The present invention describes polypeptides comprising an immunogenic
 CC part of a Mycobacterium tuberculosis antigen (Ag). Also described
 CC are vaccines and fusion protein containing M. tuberculosis Ag's.
 CC M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and
 CC other polypeptides fragments, can be used in pharmaceutical compositions
 CC or vaccines to generate a protective or therapeutic immune response to
 CC M. tuberculosis and as reagents in skin tests for diagnosis of
 CC tuberculosis. Ag can induce proliferation of, or cytokine secretion
 CC by, T, B or natural killer cells and/or macrophages in
 CC tuberculosis-immune subjects. AA219249 to AA219460 and AAY39083 to
 CC AAY39225 are used in the exemplification of the present invention.
 XX
 SQ Sequence 178 AA;
 XX
 Query Match 17.8%; Score 28; DB 20; Length 178;
 Best Local Similarity 30.8%; Pred. No. 1.8e+03;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 OY 17 PXXXXXXCXGXC 29
 | | | | |
 Db 103 PAAAAAQLCRGSC 115
 XX
 RESULT 2
 AAY39075
 ID AAY39075 standard; Protein; 178 AA.
 XX
 AC AAY39075;
 XX
 DT 05-NOV-1999 (first entry)
 XX
 DE M. tuberculosis recombinant antigen protein MO-39.
 XX
 KW Antigen; diagnosis; detection; infection; antibody; immunisation;
 KW vaccine; immunity.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO9942118-A2.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US03265.
 XX
 PR 05-MAY-1998; 98US-0072596.
 PR 18-FEB-1998; 98US-0024753.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R;
 PI Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
 XX WPI; 1999-527416/44.
 DR N-PSDB; AA219202.
 XX
 PT New polypeptide comprising antigenic portions of M. tuberculosis
 PS Example 5; Page 291; 323pp; English.
 XX
 CC This invention describes novel recombinant antigens and their encoding
 CC nucleic acids derived from Mycobacterium tuberculosis. The novel
 CC polypeptides are useful for detecting M. tuberculosis infection in a
 CC biological sample by detecting antibodies which bind with the
 CC polypeptides, and are useful as vaccines for immunizing against
 CC M. tuberculosis infection. The new detection methods are needed as
 CC current vaccination strategies do not provide 100% immunity.
 XX
 SQ Sequence 178 AA;

Query Match 17.8%; Score 28; DB 20; Length 178;
 Best Local Similarity 30.8%; Pred. No. 1.8e+03;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 OY 17 PXXXXXXCXGXC 29
 | | | | |
 Db 103 PAAAAAQLCRGSC 115
 XX
 RESULT 3
 AAO10118
 ID AAO10118 standard; Protein; 45 AA.
 XX
 AC AAO10118;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 24010.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US04927.
 XX
 PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YR, Liu C, Drmanac RT;
 PI N-PSDB; AA190049.
 DR WPI; 2001-514838/56.
 DR N-PSDB; AA190049.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX
 PS Claim 20; SEQ ID NO 24010; 1399pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibit activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 45 AA;
 XX
 Query Match 17.2%; Score 27; DB 22; Length 45;
 Best Local Similarity 30.8%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 OY 17 PXXXXXXCXGXC 29
 | | | | |
 Db 28 PASASQAQCCGTC 40

RESULT 4
AAB24498
ID AAB24498 standard; Protein: 58 AA.
XX
AC AAB24498;
XX
DT 20-NOV-2000 (first entry)
XX
DE Human secreted protein sequence encoded by gene 7 SEQ ID NO:124.
KW Human; secreted protein; cytostatic; antianaemic; antidiabetic;
KW antinflammatory; ophthalmological; antirheumatic; antiallergic;
KW antipsoriatic; antiangiogenic; cardiant; anti-HIV; neutrotropic;
KW neutrotropic; antimicrobial; antiparkinsonian; cancer;
KW immune system disorder; angiogenesis; hyperproliferative disorder;
KW cardiovascular disorder; apoptosis; neurological disease;
KW infectious disease; wound healing.
XX
OS Homo sapiens.
XX
PN MO200035937-A1.
XX
PD 22-JUN-2000.
XX
PF 16-DEC-1999; 99WO-US29950.
XX
PR 17-DEC-1998; 98US-0112809.
PR 18-DEC-1998; 98US-0113006.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Ruben SM, Ebner R, Rosen CA, Endress GA, Soppet DR, Ni J;
PI Duan DR, Moore PA, Shi Y, Lafleur DW, Olsen HS, Florence K;
XX
DR WPI: 2000-431566/37.
XX
PT Forty seven human nucleic acids encoding secreted proteins, useful in
PT the treatment, prevention and diagnosis of cancers, disorders of the
PT immune system, angiogenesis disorders, neurological diseases and
PT hyperproliferative disorders -
XX
PS Disclosure; Page 26; 562pp; English.
XX
CC The polynucleotide sequence given in AAA78381 to AAA78432 encode the
CC human secreted proteins given in AAB24437 to AAB24604. Human secreted
CC proteins have activities based on the tissues and cells the genes are
CC expressed in. Examples of activities include: cytostatic; antianaemic;
CC antidiabetic; antinflammatory; ophthalmological; antirheumatic;
CC antiallergic; antipsoriatic; antiangiogenic; cardiant; anti-HIV;
CC neutrotropic; neutrotropic; antimicrobial and antiparkinsonian.
CC Human secreted protein polynucleotides, polypeptides, antagonists and/or
CC agonists may be useful in treating, preventing, and/or diagnosing other
CC diseases, disorders, and/or conditions such as: (a) cancers; (b)
CC disorders of the immune system; (c) angiogenesis disorders; (d)
CC hyperproliferative disorders; (e) cardiovascular disorders; (f) diseases
CC associated with increase apoptosis; (g) neurological diseases; and
CC (h) infectious diseases. They are also used to promote wound healing.
CC AAA78372 to AAA78380 and AAB24436 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 58 AA;
XX
Query Match 17.2%; Score 27; DB 21; Length 58;
Best Local Similarity 30.8%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 17 PXXXXXXCXCXC 29
DB 8 PGAAAGACGAC 20

RESULT 5
ABG05086
ID ABG05086 standard; Protein: 125 AA.
XX
AC ABG05086;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #5077.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HXSE-) HXSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB; AAS69273.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID NO 35445; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 125 AA;
XX
Query Match 17.2%; Score 27; DB 22; Length 125;
Best Local Similarity 30.8%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 17 PXXXXXXCXCXC 29
DB 13 PGALLSACSGAC 25

RESULT 6
AAU19418

ID AA019418 standard; Protein; 274 AA.
 AC AA019418;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 DE Human diagnostic and therapeutic polypeptide (DITHP) #4.
 XX
 KW Human; receptor; diagnostic; therapeutic; gene therapy; vaccine;
 KW cell proliferative disorder; Crohn's disease; lymphoma; leukaemia;
 KW acquired immune deficiency syndrome; AIDS; autoimmune disorder;
 KW respiratory disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200162927-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 21-FEB-2001; 2001WO-US06059.
 XX
 PR 24-FEB-2000; 2000US-0184693.
 PR 24-FEB-2000; 2000US-0184697.
 PR 24-FEB-2000; 2000US-0184698.
 PR 24-FEB-2000; 2000US-0184768.
 PR 24-FEB-2000; 2000US-0184769.
 PR 24-FEB-2000; 2000US-0184770.
 PR 24-FEB-2000; 2000US-0184771.
 PR 24-FEB-2000; 2000US-0184772.
 PR 24-FEB-2000; 2000US-0184773.
 PR 24-FEB-2000; 2000US-0184774.
 PR 24-FEB-2000; 2000US-0184776.
 PR 24-FEB-2000; 2000US-0184777.
 PR 24-FEB-2000; 2000US-0184797.
 PR 24-FEB-2000; 2000US-0184813.
 PR 24-FEB-2000; 2000US-0184837.
 PR 24-FEB-2000; 2000US-0184841.
 PR 24-FEB-2000; 2000US-0185213.
 PR 24-FEB-2000; 2000US-0185216.
 PR 12-MAY-2000; 2000US-0203785.
 PR 15-MAY-2000; 2000US-0204226.
 PR 16-MAY-2000; 2000US-0204225.
 PR 16-MAY-2000; 2000US-0204821.
 PR 16-MAY-2000; 2000US-0204908.
 PR 16-MAY-2000; 2000US-0205232.
 PR 17-MAY-2000; 2000US-0204815.
 PR 17-MAY-2000; 2000US-0204863.
 PR 17-MAY-2000; 2000US-0205221.
 PR 17-MAY-2000; 2000US-0205285.
 PR 17-MAY-2000; 2000US-0205286.
 PR 17-MAY-2000; 2000US-0205287.
 PR 17-MAY-2000; 2000US-0205323.
 PR 17-MAY-2000; 2000US-0205324.
 XX
 PA (INCYTE GENOMICS INC.
 XX
 PI Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC;
 PI Chen A, D'Sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE;
 PI Dufour GE, Flores V, Fong WT, Greenwalt LB, Hillman JL, Jones AL;
 PI Liu TF, Roseberry AM, Rosen BH, Russo PD, Stockreher TK, Daffo A;
 PI Wright RJ, Yap PE, Yu JY, Bradley DL, Bracher SR, Chen W;
 PI Cohen HJ, Hoogson DM, Lincoln SE, Jackson S;
 XX
 DR WPI: 2001-502867/55.
 DR N-PSDB; AAS30989.
 XX
 PT Polynucleotides encoding diagnostic and therapeutic proteins, e.g.
 PT enzymes, hormones and receptors, useful in diagnostics and therapeutics
 XX
 PS Claim 27; Page 399-400; 522pp; English.
 XX
 CC The invention relates to polynucleotides (I) encoding diagnostic and

CC therapeutic (DITHP) polypeptides (II), which include e.g. enzymes,
 CC and proteins involved in growth and development and receptors. (I) and
 CC (II) may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate DITHP expression. For example, (I) and
 CC (II) may be used to treat disorders associated with decreased polypeptide
 CC expression by rectifying mutations or deletions in a patient's genome,
 CC that affect the activity of the DITHPs, by expressing inactive proteins
 CC or supplementing the patient's own production of them. (I) and (II)
 CC may be used to treat diseases, for example, cell proliferative disorder,
 CC Crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma,
 CC leukaemia, autoimmune disorders, and respiratory disorders. Additionally,
 CC (I) may be used to produce the DITHPs, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the protein. (I) and
 CC its complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids in
 CC samples, and therefore which patients may be in need of restorative
 CC therapy. (II) may also be used as antigens in the production of
 CC antibodies against DITHPs and in assays to identify modulators of DITHP
 CC expression and activity. The anti-DITHP antibodies and antagonists may
 CC also be used to down regulate expression and activity. The anti-DITHP
 CC antibodies may also be used as diagnostic agents for detecting the
 CC presence of DITHPs in samples (e.g. by enzyme linked immunosorbent
 CC assay (ELISA)). AA019415-AA019625 represent human diagnostic and
 CC therapeutic (DITHP) polypeptides of the invention.
 XX
 SQ Sequence 274 AA:
 XX
 Query Match 17.2%; Score 27; DB 22; Length 274;
 Best Local Similarity 30.8%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 17 PXXXXXXCXCXC 29
 Db 262 PCGSSSATCSGHC 274
 XX
 RESULT 7
 AAB24499
 ID AAB24499 standard; Protein; 468 AA.
 XX
 AC AAB24499;
 XX
 DT 20-NOV-2000 (first entry)
 XX
 DE Human secreted protein sequence encoded by gene 7 SEQ ID NO:125.
 XX
 KW Human; secreted protein; cytosolic; antianemic; antidiabetic;
 KW antiinflammatory; ophthalmological; antirheumatic; antiarthritic;
 KW antisporadic; antidiabetic; cardiac; anti-HIV; noctropic;
 KW neuroprotective; antimicrobial; antiparkinsonian; cancer;
 KW immune system disorder; angiogenesis; hyperproliferative disorder;
 KW cardiovascular disorder; apoptosis; neurological disease;
 KW infectious disease; wound healing.
 XX
 OS Homo sapiens.
 XX
 PN WO200035937-A1.
 XX
 PD 22-JUN-2000.
 XX
 PF 16-DEC-1999; 99WO-US29950.
 XX
 PR 17-DEC-1998; 98US-0112809.
 PR 18-DEC-1998; 98US-0113006.
 XX
 PA (HUMA-) HUMA GENOME SCI INC.
 XX
 PI Ruben SM, Ebner R, Rosen CA, Endress GA, Soppet DR, Ni J;
 PI Duan DR, Moore PA, Shi Y, Lafleur DM, Olsen HS, Florence K;
 XX
 DR WPI: 2000-431566/37.
 XX
 PT Forty seven human nucleic acids encoding secreted proteins, useful in

PT the treatment, prevention and diagnosis of cancers, disorders of the
PT immune system, angiogenesis disorders, neurological diseases and
PT hyperproliferative disorders -

PS Disclosure: Page 25-26; 562pp; English.

XX The polynucleotide sequence given in AAA78381 to AAA78432 encode the
CC human secreted proteins given in AAB24437 to AAB24604. Human secreted
CC proteins have activities based on the tissues and cells the genes are
CC expressed in. Examples of activities include: cytostatic; antineoplastic;
CC antidiabetic; antiinflammatory; ophthalmological; antirheumatic;
CC antiallergic; antipsoriatic; antiangiogenic; cardiant; anti-HIV;
CC neurotrophic; neuroprotective; antimicrobial and antiparkinsonian.
CC Human secreted protein polynucleotides, polypeptides, antagonists and/or
CC agonists may be useful in treating, preventing, and/or diagnosing other
CC diseases, disorders, and/or conditions such as: (a) cancers; (b)
CC disorders of the immune system; (c) angiogenesis disorders; (d)
CC hyperproliferative disorders; (e) cardiovascular disorders; (f) diseases
CC associated with increase apoptosis; (g) neurological diseases; and
CC (h) infectious diseases. They are also used to promote wound healing.
CC AAA78372 to AAA78380 and AAB24436 represent sequences used in the
CC exemplification of the present invention.

XX Sequence 468 AA:

Query Match 17.2%; Score 27; DB 21; Length 468;
Best Local Similarity 30.8%; Pred. No. 4.8e+03;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 17 PXXXXXXCXGXC 29
Db 8 PGAAAGACAGAC 20

RESULT 8
AAB39643
ID AAB39643 standard; Peptide: 59 AA.

XX AAB39643;

DT 04-FEB-2002 (first entry)

DE Peptide #7149 encoded by human foetal liver single exon probe.

KW Human; foetal liver; gene expression; single exon nucleic acid probe.

OS Homo sapiens.

PN WO200157277-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00669.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX Claim 27; SEQ ID NO 32278; 639pp + sequence listing; English.

CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC foetal liver. The present sequence is a peptide encoded by a single exon
CC nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 59 AA:

Query Match 16.6%; Score 26; DB 22; Length 59;
Best Local Similarity 30.8%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 17 PXXXXXXCXGXC 29
Db 20 PGSSPPSACAGAC 32

RESULT 9
AAB24324
ID AAB24324 standard; Protein: 59 AA.

XX AAB24324;

DT 23-JAN-2002 (first entry)

DE Protein #6323 encoded by probe for measuring heart cell gene expression.

KW Human; gene expression; heart; microarray; vascular system;

KW cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease.

OS Homo sapiens.

PN WO200157277-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00666.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488899/53.

XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX Claim 15; SEQ ID NO 26094; 530pp; English.

CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pcf_sequences.

XX Sequence 59 AA;

Query Match 16.6%; Score 26; DB 22; Length 59;

Best Local Similarity 30.8%; Pred. No. 1.8e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29

DB 20 PGSSPPSACAGAC 32

RESULT 10

AAM60355

ID AAM60355 standard; Protein: 59 AA.

XX AAM60355;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 32460.

XX Human: brain expressed exon; gene expression analysis; probe;

KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;

KW epilepsy; cancer.

XX Homo sapiens.

OS MO200157275-A2.

PN 09-AUG-2001.

PI 30-JAN-2001; 2001WO-US00667.

XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

DR Single exon nucleic acid probes for analyzing gene expression in human

PT brains -

XX Example 4; SEQ ID NO: 32460; 650bp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC brain. They can be used to measure gene expression in brain cell samples,

CC which may enable the diagnosis and improved treatment of nervous system

CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

CC epilepsy and cancers. The present sequence is a protein encoded by one of

CC the probes of the invention.

XX Sequence 59 AA;

Query Match 16.6%; Score 26; DB 22; Length 59;

Best Local Similarity 30.8%; Pred. No. 1.8e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29

DB 20 PGSSPPSACAGAC 32

RESULT 11

AAM72991

ID AAM72991 standard; Protein: 59 AA.

XX AAM72991;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 33297.

XX Human: bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukaemia; lymphoma; myeloma.

XX Homo sapiens.

OS MO200157276-A2.

PN 09-AUG-2001.

PI 30-JAN-2001; 2001WO-US00668.

XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

DR Human genome-derived single exon nucleic acid probes useful for

PT analyzing gene expression in human bone marrow -

XX Example 4; SEQ ID NO: 33297; 658bp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC bone marrow. They can be used to measure gene expression in bone marrow

CC samples, which may enable the improved diagnosis and treatment of cancers

CC such as lymphoma, leukemia and myeloma. The present sequence is a

CC protein encoded by one of the probes of the invention.

XX Sequence 59 AA;

Query Match 16.6%; Score 26; DB 22; Length 59;

Best Local Similarity 30.8%; Pred. No. 1.8e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29

DB 20 PGSSPPSACAGAC 32

RESULT 12

AAM19796

ID AAM19796 standard; Protein: 59 AA.

XX AAM19796;

DT 12-OCT-2001 (first entry)

DE Peptide #6230 encoded by probe for measuring cervical gene expression.

XX Probe: human; microarray; gene expression; cervical epithelial cell;

KW cervical cancer.

XX Homo sapiens.

OS

PN W0200157278-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00670.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488901/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human cervical epithelial cells -
 XX
 PS Claim 27; SEQ ID No 24622; 487bp; English.
 XX
 CC The present invention relates to human single exon nucleic acid probes
 CC (SENP: see A110068-A18459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 59 AA:
 Query Match 16.6%; Score 26; DB 22; Length 59;
 Best Local Similarity 30.8%; Pred. No. 1.8e+03;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 17 PXXXXXXXXXGXC 29
 DB 20 PGSSPPSACAGAC 32
 RESULT 13
 AAM33215
 ID AAM33215 standard; Protein; 59 AA.
 AC
 XX AAM33215;
 XX
 DT 17-OCT-2001 (first entry)
 XX
 DE Peptide #7252 encoded by probe for measuring placental gene expression.
 XX
 KW Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.
 KW
 OS Homo sapiens.
 XX
 PN W0200157272-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00663.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488897/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human placenta -
 XX
 PS Claim 27; SEQ ID No 33484; 654bp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENP:
 CC see A11315-A157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders.
 CC
 SQ Sequence 59 AA:
 Query Match 16.6%; Score 26; DB 22; Length 59;
 Best Local Similarity 30.8%; Pred. No. 1.8e+03;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 17 PXXXXXXXXXGXC 29
 DB 20 PGSSPPSACAGAC 32
 RESULT 14
 ABG42830
 ID ABG42830 standard; Peptide; 59 AA.
 AC
 XX ABG42830;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 32495.
 XX
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Rudrak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 KW
 OS Homo sapiens.
 XX
 PN W0200186003-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00665.
 XX
 PR 04-FEB-2000; 2000US-180312P.
 PR 26-MAY-2000; 2000US-207456P.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX

DR WPI: 2002-114183/15.
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples -
 XX
 PS Claim 27; SEQ ID NO 32495; 634bp; English.
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of
 CC probes; the novel set of probes which hybridise at high stringency to a
 CC nucleic acid expressed in the human lung; measuring gene expression in a
 CC sample derived from human lung, comprising (a) contacting the array with
 CC a collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of
 CC the array; identifying exons in a eukaryotic genome, comprising
 CC (a) algorithmically predicting at least one exon from genomic sequences
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene
 CC expression analysis, and for identifying exons in a gene, particularly
 CC using human lung derived mRNA and for the study of lung diseases
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
 CC Niemann-Pick disease, Hermansky-Rudrak syndrome, sarcoidosis, pulmonary
 CC haemangioendothelioma, pulmonary histiocytosis, lymphangioleiomyomatosis,
 CC pulmonary alveolar proteinosis, Karsenger syndrome, fibrocystic
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
 CC and hyaline membrane disease. The present sequence is a peptide/protein
 CC encoded by a single exon probe of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 59 AA;
 Query Match 16.6%; Score 26; DB 23; Length 59;
 Best Local Similarity 30.8%; Pred. No. 1.8e+03;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Oy 17 PXXXXXXCXGXC 29
 | | | |
 Db 20 PESSPSCACAC 32
 RESULT 15
 AAM30345
 ID AAM30345 standard; Peptide: 66 AA.
 XX
 AC AAM30345;
 XX
 DT 11-FEB-1998 (first entry)
 XX
 DE Fragment of bone morphogenic factor 3.
 XX
 XX Neururin; human; haematopoietic cell; neuronal cell; stem cell; NT gene;
 KW neurodegenerative disease; peripheral neuropathy; nervous system tumour;
 KW amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;
 KW Huntingdon's disease; ischaemic stroke; acute brain injury; basopenia;

KW acute spinal cord injury; multiple sclerosis; eosinopenia; lymphopenia;
 KW monocytopenia; neutropenia; anaemia; thrombocytopenia; neuroblastoma;
 KW antibody; obesity; therapy; bone morphogenic factor 3; growth factor;
 KW hybrid protein; BMP3.
 XX
 OS Homo sapiens.
 XX
 PN W09708196-A1.
 XX
 PD 06-MAR-1997.
 XX
 PF 27-AUG-1996; 96MO-US14065.
 XX
 PR 28-AUG-1995; 95US-0519777.
 XX
 PA (UNIV) UNIV WASHINGTON.
 XX
 PI Johnson EM, Kotzauer PT, Lampe PA, Milbrandt JD;
 XX
 DR WPI: 1997-179176/16.
 XX
 XX A novel growth factor Neururin - used to treat neuro-degenerative
 PT and haematopoietic cell degeneration diseases, e.g. Alzheimer's
 PT disease and eosinopenia
 XX
 PS Claim 93; Fig 17; 206bp; English.
 XX
 CC AAM30331-W30353 represent human growth factor fragments that are used in
 CC a hybrid polypeptide of the invention. These sequences form a hybrid
 CC with the human neururin (NT) fragment shown in AAM30378. NT promotes the
 CC growth and differentiation of haematopoietic and neuronal cells, and
 CC their stem cells. The NT gene and protein are used to prevent or treat
 CC neurodegenerative diseases e.g. peripheral neuropathy, amyotrophic
 CC lateral sclerosis, Alzheimer's disease, Parkinson's disease,
 CC Huntingdon's disease, ischaemic stroke, acute brain injury, acute spinal
 CC cord injury, nervous system tumours, multiple sclerosis and infection;
 CC and haematopoietic cell degenerative diseases, e.g. eosinopenia,
 CC basopenia, lymphopenia, monocytopenia, neutropenia, anaemia,
 CC thrombocytopenia and stem cell insufficiencies. The NT protein and gene
 CC are also useful to treat neuroblastomas. Antibodies against NT and
 CC oligonucleotides (used as either probes or primers, corresponding to an
 CC exon of pre-pro-NT gene or flanking a target sequence) can be used for
 CC detecting NT in a sample or detecting mutations in the NT gene. Antisense
 CC sequences of the NT gene are used to treat diseases promoted by NT
 CC expression e.g. obesity.
 CC
 XX
 SQ Sequence 66 AA;
 Query Match 16.6%; Score 26; DB 18; Length 66;
 Best Local Similarity 30.8%; Pred. No. 2e+03;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Oy 17 PXXXXXXCXGXC 29
 | | | |
 Db 22 PKSFDAVYCSGAC 34

Search completed: March 27, 2003, 10:59:39
 Job time : 38 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 27, 2003, 10:59:00 ; Search time 15 Seconds
(without alignments)
190.268 Million cell updates/sec

Title: US-09-828-607-6

Perfect score: 157
Sequence: 1 XXXXXXXXXXXXXXXPPYXX.....XXXXXXXXXXXXXCX 97

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	17.8	178	4	US-09-072-596-297 Sequence 297, App
2	26	16.6	103	1	US-08-335-583C-41 Sequence 41, Appl
3	26	16.6	103	3	US-08-478-097A-11 Sequence 11, Appl
4	26	16.6	103	4	US-08-931-858E-164 Sequence 164, App
5	26	16.6	103	4	US-08-981-739-164 Sequence 164, App
6	26	16.6	103	4	US-09-128-026-164 Sequence 164, App
7	26	16.6	104	1	US-08-278-729A-26 Sequence 26, Appl
8	26	16.6	104	1	US-08-155-343A-26 Sequence 26, Appl
9	26	16.6	104	1	US-08-406-672-26 Sequence 26, Appl
10	26	16.6	104	1	US-08-643-763A-26 Sequence 26, Appl
11	26	16.6	104	1	US-08-643-763A-26 Sequence 26, Appl
12	26	16.6	104	1	US-08-462-623-26 Sequence 26, Appl
13	26	16.6	104	1	US-08-451-953A-26 Sequence 26, Appl
14	26	16.6	104	2	US-08-445-468A-26 Sequence 26, Appl
15	26	16.6	104	2	US-08-461-397A-26 Sequence 26, Appl
16	26	16.6	104	2	US-08-912-088-26 Sequence 26, Appl
17	26	16.6	104	2	US-08-278-730A-26 Sequence 26, Appl
18	26	16.6	104	3	US-08-445-467-26 Sequence 26, Appl
19	26	16.6	104	3	US-08-480-515A-26 Sequence 26, Appl
20	26	16.6	104	4	US-08-271-556A-13 Sequence 13, Appl
21	26	16.6	104	4	US-09-170-936-26 Sequence 26, Appl
22	26	16.6	104	4	US-08-461-113-26 Sequence 26, Appl
23	26	16.6	104	5	PCT-US93-07190-26 Sequence 26, Appl
24	26	16.6	104	5	PCT-US93-07231-26 Sequence 26, Appl
25	26	16.6	104	5	PCT-US93-08742-26 Sequence 26, Appl
26	26	16.6	104	5	PCT-US93-08808-26 Sequence 26, Appl
27	26	16.6	104	5	PCT-US93-08885-26 Sequence 26, Appl

28	26	16.6	109	1	US-07-841-646-21 Sequence 21, Appl
29	26	16.6	109	1	US-07-901-703-17 Sequence 17, Appl
30	26	16.6	109	1	US-08-147-023-21 Sequence 21, Appl
31	26	16.6	109	1	US-08-447-570-21 Sequence 21, Appl
32	26	16.6	109	2	US-08-449-700-21 Sequence 21, Appl
33	26	16.6	109	2	US-08-449-699A-21 Sequence 21, Appl
34	26	16.6	109	5	PCT-US93-05446-17 Sequence 17, Appl
35	26	16.6	115	4	US-08-624-635-25 Sequence 25, Appl
36	26	16.6	115	4	US-08-624-635-26 Sequence 26, Appl
37	26	16.6	119	1	US-08-481-377-18 Sequence 18, Appl
38	26	16.6	119	2	US-08-491-835-16 Sequence 16, Appl
39	26	16.6	119	3	US-09-153-733A-18 Sequence 18, Appl
40	26	16.6	119	3	US-08-946-092A-16 Sequence 16, Appl
41	26	16.6	119	4	US-09-172-062-16 Sequence 16, Appl
42	26	16.6	119	4	US-09-301-520D-16 Sequence 16, Appl
43	26	16.6	119	4	US-09-389-705-18 Sequence 18, Appl
44	26	16.6	119	5	PCT-US94-00666-18 Sequence 18, Appl
45	26	16.6	119	5	PCT-US94-00685-16 Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-072-596-297
; Sequence 297, Application US/09072596
; Patent No. 6458366
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonia
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedicik, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; NUMBER OF SEQUENCES: 350
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,596
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 297:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-072-596-297
; Query Match 17.8%; Score 28; DB 4; Length 178;
; Best Local Similarity 30.8%; Pred. No. 3.4e+02;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 17 PXXXXXXCXGC 29
DB 103 PAAAAQCRGSC 115

RESULT 2
US-08-335-583C-41
Sequence 41, Application US/08335583C
Patent No. 5693779
GENERAL INFORMATION:
APPLICANT: MOOS JR., MALCOLM
APPLICANT: Wang, Shouwan
APPLICANT: Krinks, Marie
TITLE OF INVENTION: PRODUCTION AND USE OF
TITLE OF INVENTION: ANTI-DORSALIZING MORPHOGENETIC PROTEIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA: 1.5
APPLICATION NUMBER: US/08/335,583C
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH104.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
US-08-335-583C-41
Query Match 16.6%; Score 26; DB 1; Length 103;
Best Local Similarity 30.8%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 17 PXXXXXXCXGC 29
DB 22 PKSFDAYCSCGAC 34
RESULT 3
US-08-478-097A-11
Sequence 11, Application US/08478097A
Patent No. 6040431
GENERAL INFORMATION:
APPLICANT: KECK, PETER

APPLICANT: SMART, JOHN
TITLE OF INVENTION: SINGLE-CHAIN ANALOGS OF TGF-B
TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT, LLP
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,097A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESO, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-080
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..103
OTHER INFORMATION: /note="BMP3 SEQUENCE"
US-08-478-097A-11
Query Match 16.6%; Score 26; DB 3; Length 103;
Best Local Similarity 30.8%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 17 PXXXXXXCXGC 29
DB 22 PKSFDAYCSCGAC 34
RESULT 4
US-08-931-858E-164
Sequence 164, Application US/08931858E
Patent No. 6222022
GENERAL INFORMATION:
APPLICANT: JOHNSON, EUGENE M
APPLICANT: MILBRANDT, JEFFREY D
APPLICANT: KOTZBAUER, PAUL T
APPLICANT: LAMPE, PATRICIA A
APPLICANT: KLEIN, ROBERT
APPLICANT: DESAUVAGE, FRED
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858E
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-931-858E-164

Query Match 16.6%; Score 26; DB 4; Length 103;
Best Local Similarity 30.8%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29
DB 22 PKSFDAYCAGAC 34

RESULT 5
US-08-981-739-164
Sequence 164, Application US/08981739
Patent No. 6232449
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
MILBRANDT, JEFFREY D.
KOTZBAUER, PAUL T.
LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSER: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,739
FILING DATE: 31-Aug-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCW/US97/03461
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 164:
US-08-981-739-164

Query Match 16.6%; Score 26; DB 4; Length 103;
Best Local Similarity 30.8%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29
DB 22 PKSFDAYCAGAC 34

RESULT 6
US-09-128-026-164
Sequence 164, Application US/09128026
Patent No. 640335
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
MILBRANDT, JEFFREY D.
KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSER: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,026
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-128-026-164

Query Match 16.6%; Score 26; DB 4; Length 103;
Best Local Similarity 30.8%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29
DB 22 PKSFDAYCAGAC 34

RESULT 7
US-08-278-729A-26
Sequence 26, Application US/08278729A
Patent No. 5650276
GENERAL INFORMATION:
APPLICANT: SMART, JOHN
APPLICANT: OPPERMAN, HERMAN

APPLICANT: OZKAYNAK, ENGİN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,729A
FILING DATE: 20-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER Esq., EDMOND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-058CPEW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..104
OTHER INFORMATION: /label= BMP3
US-08-278-729A-26
Query Match 16.6%; Score 26; DB 1; Length 104;
Best Local Similarity 30.8%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 17 PXXXXXXCXGXC 29
DB 22 PKSFDAYCAGC 34
RESULT 8
US-08-155-343A-26
Sequence 26, Application US/08155343A
Patent No. 5656593
GENERAL INFORMATION:
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: OPPERMAN, HERMAN
APPLICANT: COHEN, CHARLES M.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE
REGENERATION.
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,343A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FENTON Esq., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-067FW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..104
OTHER INFORMATION: /label= BMP3
US-08-155-343A-26
Query Match 16.6%; Score 26; DB 1; Length 104;
Best Local Similarity 30.8%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 17 PXXXXXXCXGXC 29
DB 22 PKSFDAYCAGC 34
RESULT 9
US-08-406-672-26
Sequence 26, Application US/08406672
Patent No. 56744844
GENERAL INFORMATION:
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: COHEN, CHARLES M.
APPLICANT: OPPERMAN, HERMAN
APPLICANT: OZKAYNAK, ENGİN
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: TREATMENT TO PREVENT LOSS OF AND/OR
INCREASE BONE MASS IN METABOLIC BONE DISEASES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,672
FILING DATE: 20-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 752,857
FILING DATE: 30-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 667,274
FILING DATE: 11-MAR-1991

ATTORNEY/AGENT INFORMATION:
NAME: FENTON Esq., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-060CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7560
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..104
OTHER INFORMATION: /label= BMP3
US-08-406-672-26

Query Match 16.6%; Score 26; DB 1; Length 104;
Best Local Similarity 30.8%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29
DB 22 PKSFDAVYCSGAC 34

RESULT 10
US-08-643-563A-26

Sequence 26, Application US/08643563A
Patent No. 5707810

GENERAL INFORMATION:

APPLICANT: SMART, JOHN

APPLICANT: OPPERMAN, HERMAN

APPLICANT: OZKAYNAK, ENGIN

APPLICANT: KUBERASAMPATH, THANGAVEL

APPLICANT: RUEGER, DAVID C.

APPLICANT: PANG, ROY H.L.

APPLICANT: COHEN, CHARLES M.

TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES

STREET: 45 SOUTH STREET

CITY: HOPKINTON

STATE: MA

COUNTRY: USA

ZIP: 01748

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/643,563A

FILING DATE: 06-MAY-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: TWOMEY Esq., MICHAEL J.

REGISTRATION NUMBER: 38,349

REFERENCE/DOCKET NUMBER: CRP-058CN2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001

TELEFAX: (508) 435-6951

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

FEATURE:
NAME/KEY: Protein
LOCATION: 1..104
OTHER INFORMATION:
US-08-643-563A-26 /label= BMP3

Query Match 16.6%; Score 26; DB 1; Length 104;
Best Local Similarity 30.8%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29
DB 22 PKSFDAVYCSGAC 34

RESULT 11
US-08-643-763A-26

Sequence 26, Application US/08643763A
Patent No. 5733878

GENERAL INFORMATION:

APPLICANT: KUBERASAMPATH, THANGAVEL

APPLICANT: RUEGER, DAVID C.

APPLICANT: OPPERMAN, HERMAN

APPLICANT: COHEN, CHARLES M.

APPLICANT: PANG, ROY H.L.

TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES

STREET: 45 SOUTH STREET

CITY: HOPKINTON

STATE: MA

COUNTRY: USA

ZIP: 01748

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/643,763A

FILING DATE: 06-MAY-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: FENTON Esq., GILLIAN M.

REGISTRATION NUMBER: 36,508

REFERENCE/DOCKET NUMBER: CRP-067CN

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100

TELEFAX: (617) 248-7560

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

FEATURE:
NAME/KEY: Protein
LOCATION: 1..104
OTHER INFORMATION: /label= BMP3
US-08-643-763A-26

Query Match 16.6%; Score 26; DB 1; Length 104;
Best Local Similarity 30.8%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29
DB 22 PKSFDAVYCSGAC 34

RESULT 12
US-08-462-623-26
Sequence 26, Application US/08462623
Patent No. 5739107
GENERAL INFORMATION:
APPLICANT: COHEN, CHARLES M.
APPLICANT: CHARETTE, MARC F.
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: OPPERMAN, HERMANN
APPLICANT: PANG, ROY H.L.
APPLICANT: OKAYNAK, ENGIN
APPLICANT: SMART, JOHN E.
TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
TITLE OF INVENTION: ULCERS.
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462.623
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/445.882
FILING DATE: 22-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-074CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..104
OTHER INFORMATION: /label= BMP3
US-08-462-623-26
Query Match 16.6%; Score 26; DB 1; Length 104;
Best Local Similarity 30.8%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 17 PXXXXXXCXGC 29
| | | | |
Db 22 PKSFDAYCAGC 34

RESULT 13
US-08-451-953A-26
Sequence 26, Application US/08451953A
Patent No. 5741641
GENERAL INFORMATION:
APPLICANT: SMART, JOHN
APPLICANT: OPPERMAN, HERMANN
APPLICANT: OKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL

APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451.953A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ., EDWARD R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-058CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..104
OTHER INFORMATION: /label= BMP3
US-08-451-953A-26
Query Match 16.6%; Score 26; DB 1; Length 104;
Best Local Similarity 30.8%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 17 PXXXXXXCXGC 29
| | | | |
Db 22 PKSFDAYCAGC 34

RESULT 14
US-08-445-468A-26
Sequence 26, Application US/08445468A
Patent No. 5849686
GENERAL INFORMATION:
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: OPPERMAN, HERMANN
APPLICANT: PANG, ROY H.L.
APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: MORPHOGEN-INDUCED LIVER REGENERATION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,468A
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-072FW2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..104
OTHER INFORMATION: /label= BMP3
US-08-445-468A-26

Query Match 16.6% Score 26; DB 2; Length 104;
Best Local Similarity 30.8%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXKXGXC 29
DB 22 PKSPDAYCAGAC 34

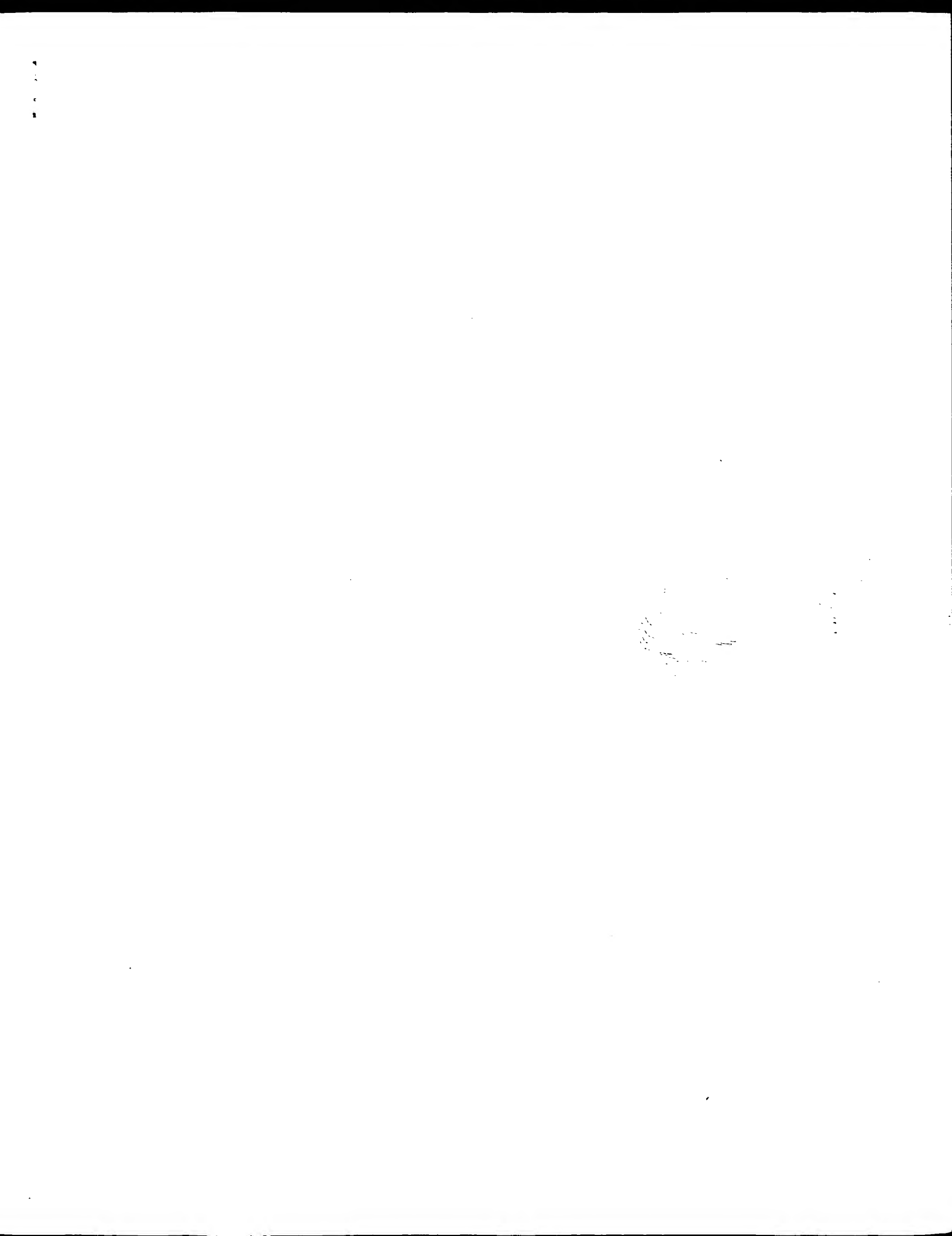
RESULT 15
US-08-461-397A-26
Sequence 26; Application US/08461397A
Patent No. 5972884
GENERAL INFORMATION:
APPLICANT: COHEN, CHARLES M.
APPLICANT: CHARETTE, MARC F.
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUGGER, DAVID C.
APPLICANT: OPPERMAN, HERMANN
APPLICANT: PANG, ROY H.L.
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: SMART, JOHN E.
TITLE OF INVENTION: MORPHOGEN TREATMENT FOR LIMITING
TITLE OF INVENTION: PROLIFERATION OF EPITHELIAL CELLS.
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,397A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ., EDWARD R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-074FW2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..104
OTHER INFORMATION: /label= BMP3
US-08-461-397A-26

Query Match 16.6% Score 26; DB 2; Length 104;
Best Local Similarity 30.8%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXKXGXC 29
DB 22 PKSPDAYCAGAC 34

Search completed: March 27, 2003, 11:02:54
Job time : 16 secs



GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 27, 2003, 10:59:45 ; Search time 14 Seconds

(Without alignments)
406,871 Million cell updates/sec

Title: US-09-828-607-6

Perfect score: 157
Sequence: 1 XX 97Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, AA:*

1: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubppa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	17.2	549	10	US-09-801-368-358
2	27	17.2	2609	9	US-10-184-644-407
3	27	17.2	2870	9	US-10-184-644-473
4	26	16.6	59	10	US-09-864-761-39622
5	26	16.6	84	10	US-09-995-515-8
6	26	16.6	115	10	US-09-813-459-25
7	26	16.6	115	10	US-09-813-459-26
8	26	16.6	119	12	US-10-115-406-16
9	26	16.6	120	9	US-09-859-211-42
10	26	16.6	120	9	US-09-880-708-20
11	26	16.6	120	10	US-09-813-459-6
12	26	16.6	120	10	US-09-813-459-16
13	26	16.6	131	10	US-09-995-515-12
14	26	16.6	140	10	US-09-995-515-2
15	26	16.6	182	9	US-09-974-879-139
16	26	16.6	195	10	US-09-995-515-4
17	26	16.6	212	9	US-09-949-192-29
18	26	16.6	473	9	US-09-813-398-25
19	26	16.6	476	10	US-09-813-459-5

20	26	16.6	479	9	US-09-813-398-26	Sequence 26, Appl
21	26	16.6	2121	9	US-10-184-644-355	Sequence 355, Appl
22	26	16.6	4440	9	US-10-174-590-525	Sequence 525, Appl
23	26	16.6	4440	9	US-10-176-758-525	Sequence 525, Appl
24	26	16.6	4440	9	US-10-175-737-525	Sequence 525, Appl
25	26	16.6	4440	9	US-10-173-706-525	Sequence 525, Appl
26	26	16.6	4440	9	US-10-175-738-525	Sequence 525, Appl
27	26	16.6	4440	9	US-10-175-752-525	Sequence 525, Appl
28	26	16.6	4440	9	US-10-176-487-525	Sequence 525, Appl
29	26	16.6	4440	9	US-10-176-757-525	Sequence 525, Appl
30	26	16.6	4440	9	US-10-176-913-525	Sequence 525, Appl
31	26	16.6	4440	9	US-10-180-552-525	Sequence 525, Appl
32	26	16.6	4440	9	US-10-180-557-525	Sequence 525, Appl
33	26	16.6	4440	9	US-10-173-700-525	Sequence 525, Appl
34	26	16.6	4440	9	US-10-174-572-525	Sequence 525, Appl
35	26	16.6	4440	9	US-10-174-579-525	Sequence 525, Appl
36	26	16.6	4440	9	US-10-174-582-525	Sequence 525, Appl
37	26	16.6	4440	9	US-10-174-588-525	Sequence 525, Appl
38	26	16.6	4440	9	US-10-175-739-525	Sequence 525, Appl
39	26	16.6	4440	9	US-10-175-740-525	Sequence 525, Appl
40	26	16.6	4440	9	US-10-175-743-525	Sequence 525, Appl
41	26	16.6	4440	9	US-10-176-488-525	Sequence 525, Appl
42	26	16.6	4440	9	US-10-176-492-525	Sequence 525, Appl
43	26	16.6	4440	9	US-10-176-747-525	Sequence 525, Appl
44	26	16.6	4440	9	US-10-176-750-525	Sequence 525, Appl
45	26	16.6	4440	9	US-10-176-985-525	Sequence 525, Appl

ALIGNMENTS

RESULT 1
US-09-801-368-358
Sequence 358, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. US20020128250A1man, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 358
LENGTH: 549
TYPE: PRT
ORGANISM: Aspergillus nidulans
US-09-801-368-358

Query Match 17.2% Score 27; DB 10; Length 549;
Best Local Similarity 30.8%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
DB 168 PAVTSGCTGSC 180

RESULT 2

US-10-184-644-407

Sequence 407, Application US/10184644
Publication No. US20030044930A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 407
LENGTH: 2609
TYPE: DNA
ORGANISM: Homo Sapien
US-10-184-644-407

Query Match 17.2%; Score 27; DB 9; Length 2609;
Best Local Similarity 10.5%; Pred. No. 4.3e+03;
Matches 4; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 25 CXGXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 62

Db 2393 CCGCTGTCATTTGAGTATTTTAAAAAATATGTC 2430

RESULT 3

US-10-184-644-473

Sequence 473, Application US/10184644
Publication No. US20030044930A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 473
LENGTH: 2870
TYPE: DNA
ORGANISM: Homo Sapien
US-10-184-644-473

Query Match 17.2%; Score 27; DB 9; Length 2870;
Best Local Similarity 10.5%; Pred. No. 4.6e+03;
Matches 4; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 25 CXGXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 62

Db 2823 CCGCTTTACTTTAACTGATATTAATATATATC 2860

RESULT 4

US-09-864-761-39622

Sequence 39622, Application US/09864761
Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 39622
LENGTH: 59
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005809.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.5
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 66
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.1
OTHER INFORMATION: SWISSPROT HIT: 076942, EVALUUE 1.60e+00
US-09-864-761-39622

Query Match 16.6%; Score 26; DB 10; Length 59;
Best Local Similarity 30.8%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGC 29
DB 20 PGSSPPSACAGAC 32

RESULT 5

US-09-995-515-8
; Sequence 8, Application US/09995515
; Patent No. US20020151695A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shugian
; TITLE OF INVENTION: Transforming Growth Factor-Beta-Related Molecules and
; FILE REFERENCE: 00-659-7
; CURRENT APPLICATION NUMBER: US/09/995,515
; PRIOR FILING DATE: 2001-11-28
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-995-515-8

Query Match 16.6%; Score 26; DB 10; Length 84;
Best Local Similarity 30.8%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGC 29
DB 56 PRTLSFYCQCTC 68

RESULT 6

US-09-813-459-25
; Sequence 25, Application US/09813459
; Patent No. US20020107369A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Judas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,459
; FILING DATE: 20-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/624,635
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Wehertell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-3054
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100

TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: Human GDF-10

FEATURE:
NAME/KEY: protein
LOCATION: 1..115

US-09-813-459-25
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Query Match 16.6%; Score 26; DB 10; Length 115;
Best Local Similarity 30.8%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGC 29
DB 34 PXSFDATYCAGAC 46

RESULT 7

US-09-813-459-26
; Sequence 26, Application US/09813459
; Patent No. US20020107369A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Judas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,459
; FILING DATE: 20-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/624,635
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Wehertell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-3054
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: Murine GDF-10
; FEATURE:
NAME/KEY: protein
LOCATION: 1..115
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-813-459-26

Query Match
Best Local Similarity 16.6%; Score 26; DB 10; Length 115;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29
DB 34 PKSFDAVYCSGAC 46

RESULT 8

US-10-115-406-16
Sequence 16, Application US/10115406
Patent No. US20020127612A1
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: Lee, Se-jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
FILE REFERENCE: JH01190-3
CURRENT APPLICATION NUMBER: US/10/115,406
CURRENT FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 09/301,520
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: US 09/172,062
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 08/491,835
PRIOR FILING DATE: 1995-10-23
PRIOR APPLICATION NUMBER: PCT/US94/00685
PRIOR FILING DATE: 1994-01-12
PRIOR APPLICATION NUMBER: US 08/003,303
PRIOR FILING DATE: 1993-01-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
US-10-115-406-16

Query Match
Best Local Similarity 16.6%; Score 26; DB 12; Length 119;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29
DB 38 PKSFDAVYCSGAC 50

RESULT 9

US-09-859-211-42
Sequence 42, Application US/09859211
Patent No. US20020157125A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/14401
CURRENT APPLICATION NUMBER: US/09/859,211
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 08/862,445
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/525,596
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR FILING DATE: 1994-03-18
PRIOR APPLICATION NUMBER: 08/033,923

PRIOR FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 42
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens
US-09-859-211-42

Query Match
Best Local Similarity 16.6%; Score 26; DB 9; Length 120;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29
DB 39 PKSFDAVYCSGAC 51

RESULT 10

US-09-880-708-20
Sequence 20, Application US/09880708
Patent No. US20020165361A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92121-2189
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/880,708
FILING DATE: 12-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/145,060
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Helle, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
TELEFAX: 619/677-1465
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: BMP-3
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-880-708-20

Query Match
Best Local Similarity 16.6%; Score 26; DB 9; Length 120;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29
DB 39 PKSFDAVYCSGAC 51

RESULT 11
US-09-813-459-6
Sequence 6, Application US/09813459
Patent No. US20020107369A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
Cunningham, No. US20020107369A1
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/813,459
APPLICATION NUMBER: US/09/813,459
FILING DATE: 20-Mar-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/624,635
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.,
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-3054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GDF-10
FEATURE:
NAME/KEY: Protein
LOCATION: 1..120
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-813-459-6
Query Match 16.6%; Score 26; DB 10; Length 120;
Best Local Similarity 30.8%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 17 PXXXXXXCXGC 29
DB 39 PKSFDAVYCAGC 51
RESULT 12
US-09-813-459-16
Sequence 16, Application US/09813459
Patent No. US20020107369A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
Cunningham, No. US20020107369A1
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles

STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/813,459
APPLICATION NUMBER: US/09/813,459
FILING DATE: 20-Mar-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/624,635
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.,
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-3054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: BMP-3
FEATURE:
NAME/KEY: Protein
LOCATION: 1..120
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-813-459-16
Query Match 16.6%; Score 26; DB 10; Length 120;
Best Local Similarity 30.8%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 17 PXXXXXXCXGC 29
DB 39 PKSFDAVYCAGC 51
RESULT 13
US-09-995-515-12
Sequence 12, Application US/09995515
Patent No. US20020151695A1
GENERAL INFORMATION:
APPLICANT: Jing, Shuguan
TITLE OF INVENTION: Transforming Growth Factor-Beta-Related Molecules and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-659-A
CURRENT APPLICATION NUMBER: US/09/995,515
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 60/253,476
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 131
TYPE: PRT
ORGANISM: Homo sapiens
US-09-995-515-12
Query Match 16.6%; Score 26; DB 10; Length 131;
Best Local Similarity 30.8%; Pred. No. 8.6e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 17 PXXXXXXCXGC 29

Db 103 PKTISFYCGTC 115

RESULT 14

US-09-995-515-2

; Sequence 2, Application US/09995515

; Patent No. US20020151695A1

; GENERAL INFORMATION:

; APPLICANT: Jing, Shugian

; TITLE OF INVENTION: Transforming Growth Factor-Beta-Related Molecules and

; FILE REFERENCE: 00-659-A

; CURRENT APPLICATION NUMBER: US/09/995,515

; CURRENT FILING DATE: 2001-11-28

; PRIOR APPLICATION NUMBER: 60/253,476

; PRIOR FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO 2

; LENGTH: 140

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-995-515-2

Query Match 16.6%; Score 26; DB 10; Length 140;

Best Local Similarity 30.8%; Pred. No. 9e+02;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGC 29

Db 64 PKTISFYCGTC 76

RESULT 15

US-09-974-879-139

; Sequence 139, Application US/09974879

; Publication No. US20030028003A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 125 Human Secreted Proteins

; FILE REFERENCE: P020P2

; CURRENT APPLICATION NUMBER: US/09/974,879

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: US 60/239,893

; PRIOR FILING DATE: 2000-10-13

; PRIOR APPLICATION NUMBER: US 09/818,683

; PRIOR FILING DATE: 2001-03-28

; PRIOR APPLICATION NUMBER: US 09/305,736

; PRIOR FILING DATE: 1999-05-05

; PRIOR APPLICATION NUMBER: PCT/US98/23435

; PRIOR FILING DATE: 1998-11-04

; PRIOR APPLICATION NUMBER: US 60/064,911

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: US 60/064,912

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: US 60/064,983

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: US 60/064,900

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: US 60/064,988

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: US 60/064,987

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: US 60/064,908

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: US 60/064,984

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: US 60/064,985

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: US 60/066,094

; PRIOR FILING DATE: 1997-11-17

; PRIOR APPLICATION NUMBER: US 60/066,100

; PRIOR FILING DATE: 1997-11-17

; PRIOR APPLICATION NUMBER: US 60/066,089

; PRIOR FILING DATE: 1997-11-17

; PRIOR APPLICATION NUMBER: US 60/066,095

; PRIOR FILING DATE: 1997-11-17

; PRIOR APPLICATION NUMBER: US 60/066,090

; PRIOR FILING DATE: 1997-11-17

; NUMBER OF SEQ ID NOS: 611

; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO 139

; LENGTH: 182

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-974-879-139

Query Match 16.6%; Score 26; DB 9; Length 182;

Best Local Similarity 30.8%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGC 29

Db 153 PTVLYTSACLGIC 165

Search completed: March 27, 2003, 11:03:15

Job time: 14 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 27, 2003, 10:58:19 ; Search time 44 Seconds

(without alignments)
211.933 Million cell updates/sec

Title: US-09-828-607-6

Perfect score: 157
Sequence: 1 XXXXXXXXXXXXXXXXXXXXXXXXXX.XXXXXXXXXXXXXXXXXXXXXX 97

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

PIR.73:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	17.2	967	2	G86229 hypothetical prote
2	26	16.6	119	2	S48192 insulin-like growt
3	26	16.6	278	2	T20478 hypothetical prote
4	26	16.6	347	2	T24528 hypothetical prote
5	26	16.6	360	2	I53032 bone morphogenetic
6	26	16.6	470	2	B83991 glycolate oxidase
7	26	16.6	472	1	BMH03 bone morphogenetic
8	26	16.6	476	2	JC4646 bone morphogenetic
9	26	16.6	478	2	JC4838 bone morphogenetic
10	26	16.6	598	2	T02795 P-glycoprotein - r
11	25	15.9	99	2	S22351 transforming growt
12	25	15.9	112	2	A61439 transforming growt
13	25	15.9	240	2	T45814 hypothetical prote
14	25	15.9	366	2	T03907 TGF-beta-related p
15	25	15.9	407	2	H84920 probable TUB fami
16	25	15.9	407	2	T37242 transforming growt
17	25	15.9	412	2	A39489 transforming growt
18	25	15.9	413	1	WFXL2 transforming growt
19	25	15.9	414	1	WFKB2 transforming growt
20	25	15.9	414	1	WFKB2 transforming growt
21	25	15.9	414	1	A31249 transforming growt
22	25	15.9	442	2	B31249 transforming growt
23	25	15.9	470	2	D69984 glycolate oxidase
24	25	15.9	553	1	A42459 millerian inhibiti
25	25	15.9	553	1	S20100 millerian inhibiti
26	25	15.9	563	2	T20192 hypothetical prote
27	25	15.9	575	1	WFBOM millerian inhibiti
28	25	15.9	575	1	T11753 millerian inhibiti
29	25	15.9	612	2	G83307 hypothetical prote

30	25	15.9	885	1	A55453 nucleotide diphosp
31	25	15.9	889	2	E87304 TonB-dependent rec
32	25	15.9	1574	2	T13954 ME66 protein - ra
33	24	15.3	20	2	I67551 monocytic chemotact
34	24	15.3	25	2	JH0701 omega-conotoxin MY
35	24	15.3	25	2	JH0700 omega-conotoxin MY
36	24	15.3	27	2	C44379 omega-conotoxin SV
37	24	15.3	26	2	S55030 CAP5 protein - ant
38	24	15.3	29	2	JH0699 omega-conotoxin MY
39	24	15.3	29	2	A58537 omega-conotoxin MY
40	24	15.3	41	2	A59149 sigma-conotoxin GV
41	24	15.3	43	2	S18173 metallothionein -
42	24	15.3	43	2	S18174 metallothionein -
43	24	15.3	43	2	S3382 conotoxin-like pro
44	24	15.3	52	2	T10299 conotoxin homolog
45	24	15.3	53	2	C72850

ALIGNMENTS

RESULT 1

G86229

hypothetical protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: G86229

R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luro, J.S.; Malt, R.; Marzla

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: G86229

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-967 <STO>

A:Cross-references: GB:AE005172; NID:93482933; PIDN:AC33218.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match

Best Local Similarity 30.8%;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGC 29
Db 726 PQETRRSRGAC 738

RESULT 2

S48192 insulin-like growth factor S11 precursor - soybean

N:Alternate names: leginsulin

C:Species: Glycine max (soybean)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Oct-2000

C:Accession: S48192; PNO116

R:Matanabe, Y.; Barbashov, S.F.; Komatsu, S.; Hemmings, A.M.; Miyagi, M.; Tsunawasa,

Eur. J. Biochem. 224, 167-172, 1994

A:Title: A peptide that stimulates phosphorylation of the plant insulin-binding prote

A:Reference number: S48192; MUID:94357216; PMID:8076638

A:Accession: S48192

A:Molecule type: mRNA; protein

A:Residues: 1-119 <WAT>

A:Cross-references: GB:DL7996; NID:9498167; PIDN:BA04219.1; PTD:9498168

Mol. Biol. (Mosk.) 24, 953-961, 1990

A:Title: Using monoclonal antibodies to insulin for isolating proteins inhibiting cel

A:Reference number: PN0115; MUID:91066897; PMID:2250683

A:Accession: PN0116

A:Molecule type: protein

A:Residues: 20-30, 'W', '32-39 <BAR>

F:1-19/Domain: propeptide #status predicted <PRO>

F:20-56/Product: insulin-like growth factor sII #status experimental <MAT>

Query Match 16.6%; Score 26; DB 2; Length 119;

Best Local Similarity 30.8%; Pred. No. 6.9e+02;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29

DB 14 PTKIEMADCGAC 26

RESULT 3

T20478 hypothetical protein F01G10.6 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T20478

R:Hemby, C. submitted to the EMBL Data Library, October 1996

A:Reference number: Z19280

A:Accession: T20478

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-278 <MIL>

A:Cross-references: EMBL:Z81055; PIDN:GAB02894.1; GSPDB:GN00022; CESP:F01G10.6

A:Experimental source: clone F01G10

C:Genetics:

A:Gene: CESP:F01G10.6

A:Map position: 4

A:Introns: 84/1; 168/1

Query Match 16.6%; Score 26; DB 2; Length 278;

Best Local Similarity 30.8%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29

DB 59 PSNTFAESCSGPC 71

RESULT 4

T24528 hypothetical protein T05E12.1 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T24528

R:McMurray, A. submitted to the EMBL Data Library, November 1996

A:Reference number: Z19904

A:Accession: T24528

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-347 <MIL>

A:Cross-references: EMBL:Z81585; PIDN:GAB04681.1; GSPDB:GN00023; CESP:T05E12.1

A:Experimental source: clone T05E12

C:Genetics:

A:Gene: CESP:T05E12.1

A:Map position: 5

A:Introns: 61/3; 90/1; 165/2; 187/3; 256/3

Query Match 16.6%; Score 26; DB 2; Length 347;

Best Local Similarity 30.8%; Pred. No. 1.3e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29

DB 87 PLIATTSCTGCLC 99

RESULT 5

I53032 bone morphogenetic protein 3 - rat (fragment)

C:Species: *Rattus sp.* (rat)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999

C:Accession: I53032

R:Chen, D.; Feng, J.Q.; Feng, M.; Harris, M.A.; Mahy, P.; Mundy, G.R.; Harris, S.E.

DNA Cell Biol. 14, 235-239, 1995

A:Title: Sequence and expression of bone morphogenetic protein 3 mRNA in prolonged cu

A:Reference number: I53032; MUID:95186061; PMID:7860444

A:Accession: I53032

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Cross-references: GB:S77492; NID:9957225; PIDN:AAB33725.1; PID:9957226

C:Superfamily: Inhibin

Query Match 16.6%; Score 26; DB 2; Length 360;

Best Local Similarity 30.8%; Pred. No. 1.4e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29

DB 279 PKSFDAYYCSGAC 291

RESULT 6

B83991 glycolate oxidase subunit BH2730 [imported] - *Bacillus halodurans* (strain C-125)

C:Species: *Bacillus halodurans*

C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C:Accession: B83991

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* a

A:Reference number: A83650; MUID:2051582; PMID:11058132

A:Accession: B83991

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-470 <STO>

A:Cross-references: GB:AP001516; GB:BA000004; NID:910175192; PIDN:BAB06449.1; GSPDB:G

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH2730

C:Superfamily: glycolate oxidase chain glycd

Query Match 16.6%; Score 26; DB 2; Length 470;

Best Local Similarity 30.8%; Pred. No. 1.6e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29

DB 69 PRSGTNLCAGTC 81

RESULT 7

BMHU3 bone morphogenetic protein 3 precursor - human

N:Alternate names: osteogenin

C:Species: *Homo sapiens* (man)

C>Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999

C:Accession: D37278

R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mltsock, L.M.; Whitters, M.J.; Kile, R.W.;

Science 242, 1528-1534, 1988

A:Title: Novel regulators of bone formation: molecular clones and activities.

A:Reference number: A37278; MUID:89072730; PMID:3201241

A:Accession: D37278

A:Molecule type: mRNA

A:Residues: 1-472 <WO4>

A:Cross-references: GB:M22491; NID:g179505; PIDN:AAA51836.1; PID:g179506

C:Genetics: GDB:BMP3

A:Cross-references: GDB:125206; OMIM:112263
A:Map position: 4p14-4q21

C:Superfamily: Inhibin

C:Keywords: bone; glycoprotein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-345/Domain: propeptide #status predicted <PRO>

F:346-472/Product: bone morphogenetic protein 3 #status predicted <MAT>

F:117,141,175,220,463/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.6%; Score 26; DB 1; Length 472;

Best Local Similarity 30.8%; Pred. No. 1.6e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29

DB 391 PKSFDAVYCSGAC 403

RESULT 8

JC4646 bone morphogenetic protein-3b precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 01-Dec-2000

C:Accession: JC4646

R:Takao, M.; Hino, J.; Takeshita, N.; Konno, Y.; Nishizawa, T.; Matsuo, H.; Kangawa, K.

Biochem. Biophys. Res. Commun. 219, 656-662, 1996

A:Title: Identification of rat bone morphogenetic protein-3b (BMP-3b), a new member of B

A:Reference number: JC4646; MUID:96133707; PMID:8605043

A:Accession: JC4646

A:Molecule type: mRNA

A:Residues: 1-476 <TAK>

A:Cross-references: DDBJ:DA9494; NID:9699625; PIDN:BA08454.1; PID:9699626

A:Experimental source: femur

C:Comment: This protein plays a role in the central nervous system as well as in new bon

acellular matrix.

C:Superfamily: Inhibin

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-366/Domain: propeptide #status predicted <PRO>

F:367-476/Product: bone morphogenetic protein-3b #status predicted <MAT>

F:114,152,277,467/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.6%; Score 26; DB 2; Length 476;

Best Local Similarity 30.8%; Pred. No. 1.6e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29

DB 395 PKSFDAVYCSGAC 407

RESULT 9

JC4838 bone morphogenetic protein-3b precursor [similarity] - human

N:Alternate names: BMP-3b; GDF-10

C:Species: Homo sapiens (man)

C>Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 01-Dec-2000

C:Accession: JC4838

R:Hino, J.; Takao, M.; Takeshita, N.; Konno, Y.; Nishizawa, T.; Matsuo, H.; Kangawa, K.

Biochem. Biophys. Res. Commun. 223, 304-310, 1996

A:Title: cDNA cloning and genomic structure of human bone morphogenetic protein-3b (BMP-

A:Reference number: JC4838; MUID:96264636; PMID:8670277

A:Accession: JC4838

A:Molecule type: mRNA

A:Residues: 1-478 <HIN>

A:Cross-references: DDBJ:DA9492; NID:9699603; PIDN:BA08452.1; PID:9699604

C:Comment: This protein induces endochondral bone formation, chemotaxis of monocytes, an

C:Genetics:

A:Gene: bmp-3b

C:Superfamily: Inhibin

C:Keywords: bone

F:1-33/Domain: signal sequence #status predicted <SIG>

F:34-368/Domain: propeptide #status predicted <PRO>

F:369-478/Product: bone morphogenetic protein-3b #status predicted <MAT>

Query Match 16.6%; Score 26; DB 2; Length 478;

Best Local Similarity 30.8%; Pred. No. 1.6e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29

DB 397 PKSFDAVYCSGAC 409

RESULT 10

T02795 probable membrane protein L549.7 [Imported] - Leishmania major (strain Friedlin)

C:Species: Leishmania major

C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000

C:Accession: G81455; T02795

R:Myler, P.V.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C

Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999

A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protel

A:Reference number: A81455; MUID:99178987; PMID:10077609

A:Accession: G81455

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-598 <PYL>

A:Cross-references: GB:AE001274; NID:93264850; PIDN:AC24619.1; PID:92978456; GSPDB:C

A:Experimental source: strain MNOM/IL/61/Friedlin

C:Genetics:

A:Gene: L549.7

A:Map position: 1

C:Superfamily: Leishmania major probable membrane protein L549.7

C:Keywords: transmembrane protein

Query Match 16.6%; Score 26; DB 2; Length 598;

Best Local Similarity 30.8%; Pred. No. 1.9e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29

DB 96 PSSSSSGCGPGCG 108

RESULT 11

P-glycoprotein - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999

C:Accession: S22351

R:Deuchars, K.L.; Duttle, M.; Ling, V.

Biochim. Biophys. Acta 1130, 157-165, 1992

A:Title: Identification of distinct P-glycoprotein gene sequences in rat.

A:Reference number: S22351; MUID:92223089; PMID:1348630

A:Accession: S22351

A:Molecule type: DNA

A:Residues: 1-99 <DEU>

A:Cross-references: EMBL:X61106; NID:956800; PIDN:CAA43418.1; PID:e39738; PID:g133421

A>Note: the authors translated the codon TTC for residue 48 as Leu

A>Note: the authors did not translate the codon for residue 99

C:Keywords: glycoprotein

Query Match 15.9%; Score 25; DB 2; Length 99;

Best Local Similarity 30.8%; Pred. No. 8.8e+02;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29

DB 42 PSVTALFLCFGRG 54

RESULT 12

A61439

transforming growth factor beta-2 - bovine

N:Alternate names: cartilage-inducing factor B; MGF-a; milk growth factor a
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
 C:Accession: A61439; A25485; B42320; S15389
 R:Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.
 J. Protein Chem. 10, 565-575, 1991
 A:Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta
 A:Reference number: A61439; PMID:92189724; PMID:1799413
 A:Accession: A61439
 A:Molecule type: protein
 A:Residues: 1-112 <PIN>
 A:Experimental source: milk
 R:Sejedin, S.M.; Segarini, P.R.; Rosen, D.M.; Thompson, A.V.; Bentz, H.; Graycar, J.
 J. Biol. Chem. 262, 1946-1949, 1987
 A:Title: Cartilage-inducing factor-B is a unique protein structurally and functionally
 A:Reference number: A25485; PMID:87137406; PMID:3469199
 A:Accession: A25485
 A:Molecule type: protein
 A:Residues: 1-30 <SEY>
 A:Experimental source: bone
 R:Ogawa, Y.; Schmidt, D.K.; Dasch, J.R.; Chang, R.J.; Glaser, C.B.
 J. Biol. Chem. 267, 2325-2328, 1992
 A:Title: Purification and characterization of transforming growth factor-beta2.3 and -b
 A:Reference number: A42320; PMID:92129307; PMID:1733936
 A:Accession: B42320
 A:Molecule type: protein
 A:Residues: 1-6, 'X', 8-14, 'XX', 17-34 <OGA>
 A:Experimental source: bone
 R:Cox, D.A.; Buerk, R.R.
 Eur. J. Biochem. 197, 353-358, 1991
 A:Title: Isolation and characterization of milk growth factor, a transforming growth fac
 A:Reference number: S15389; PMID:91224126; PMID:2026157
 A:Accession: S15389
 A:Molecule type: protein
 A:Residues: 1-16, 'XX', 19 <COX>
 A:Experimental source: milk
 C:Superfamily: inhibin
 C:Keywords: growth factor; growth regulation; heterodimer; homodimer

Query Match 15.9%; Score 25; DB 2; Length 112;
 Best Local Similarity 30.8%; Pred. No. 9.6e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29
 DB 36 PKGYNNFCAGAC 48

RESULT 13
 T45814
 hypothetical protein F2809.210 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
 C:Accession: T45814
 R:Benes, V.; Rechmann, S.; Borkova, D.; Ansoerge, W.; Meves, H.W.; Lemcke, K.; Mayer, K.F.
 submitted to the Protein Sequence Database, January 2000
 A:Reference number: Z23014
 A:Accession: T45814
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-240 <BEN>
 A:Cross-references: EMBL:AL137080
 A:Experimental source: cultivar Columbia; BAC clone F2809
 C:Genetics:
 A:Map position: 3
 A:Introns: 38/2; 82/2; 123/2; 196/2
 A:Note: F2809.210

Query Match 15.9%; Score 25; DB 2; Length 240;
 Best Local Similarity 30.8%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29

DB 136 PGEESACAGEC 148

RESULT 14
 T03907
 TGF-beta-related protein homolog F3963.8 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 17-Mar-2000
 C:Accession: T03907
 R:Du, Z.; Le, T.T.; Holmes, A.
 submitted to the EMBL Data Library, July 1997
 A:Description: The sequence of C. elegans cosmid F3963.
 A:Reference number: Z15131
 A:Accession: T03907
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-366 <DUZ>
 A:Cross-references: EMBL:AF016424; NID:g2291203; PIDN:AAB65333.1; PID:g2291211
 C:Genetics:
 A:Map position: V
 A:Introns: 38/2; 86/2; 110/1; 161/2; 205/1; 229/2; 259/1
 A:Note: F3963.8
 C:Superfamily: inhibin

Query Match 15.9%; Score 25; DB 2; Length 366;
 Best Local Similarity 30.8%; Pred. No. 2e+03;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29
 DB 286 PEGSAPYCSGDC 298

RESULT 15
 H84920
 probable Tubb family protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: H84920
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; PMID:20083487; PMID:10617197
 A:Accession: H84920
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-407 <STO>
 A:Cross-references: GB:AE002093; NID:g3738302; PIDN:AAC63644.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g47900
 A:Map position: 2

Query Match 15.9%; Score 25; DB 2; Length 407;
 Best Local Similarity 30.8%; Pred. No. 2.1e+03;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29
 DB 75 PSRRNVSCAGVC 87

Search completed: March 27, 2003, 11:02:33
 Job time : 45 secs

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: AF042381; AAC38334.1; -
 CC EMBL: AE013388; AAM31239.1; -
 DR TIGRAME: TIGR01111; mtra; 1.
 KW transferase; Methyltransferase; Methanogenesis; Cobalt.
 FT BINDING 85 85
 FT 5-HYDROXYBENZIMIDAZOL COBAMIDE COFACTOR
 FT (BY SIMILARITY).
 FT POLY-GLU.
 FT DOMAIN 169 176
 FT 232 238
 FT POLY-LEU.
 FT 16 16
 FT G -> R (IN REF. 1).
 FT 71 71
 FT N -> D (IN REF. 1).
 FT 127 127
 FT E -> G (IN REF. 1).
 FT 161 161
 FT D -> E (IN REF. 1).
 SQ SEQUENCE 240 AA; 25366 MW; 44C086DD3561E526 CRC64;

Query Match 17.2%; Score 27; DB 1; Length 240;
 Best Local Similarity 30.8%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29
 DB 40 PILDAGAACTGSC 52

RESULT 2

ALBL_GLYSO STANDARD; PRT; 119 AA.

AC 0920X0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Albumin 1 precursor (PAL) [contains: PALA; Leginsulin (PALB)].
 OS Glycine soja.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosidia I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 RX NCBI_TaxID=3848;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Tan J.Z., Lou C.F., Hirano H.;
 RT "Analysis of leginsulin gene in soybean cultivar (glycine max) and
 RT wild species (glycine soja)."
 RL Chin. J. Appl. Environ. Biol. 5:259-263(1999).
 CC -1- FUNCTION: LEGINSULIN BINDS TO BASIC 7S GLOBULIN (BG) AND
 CC STIMULATES ITS PHOSPHORYLATION ACTIVITY (BY SIMILARITY).
 CC -1- PTM: THREE DISULFIDE BONDS ARE PROBABLY PRESENT.
 CC -1- PTM: THE C-TERMINAL GLYCINE MAY BE REMOVED FROM LEGINSULIN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: AJ011935; CAA09880.2; -
 KW Seed storage protein; Albumin; Signal.
 FT SIGNAL 1 19
 FT 19
 FT CHAIN 20 56
 FT 57 64
 FT PROPEP 65 117
 FT 118 119
 FT 119 AA; 12963 MW; EE5457D8D09070CC CRC64;

Query Match 16.6%; Score 26; DB 1; Length 119;
 Best Local Similarity 30.8%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29

DB 14 PTKIEADDCGAC 26

RESULT 3

ALBL_SOYBN STANDARD; PRT; 119 AA.

AC 039837; O49854;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Albumin 1 precursor (PAL) [contains: PALA; Leginsulin (PALB)].
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosidia I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 RX NCBI_TaxID=3847;
 RN [1]

RP SEQUENCE FROM N.A.
 RA STRAIN-cv. Miyagishihrome; TISSUE-Radicle;
 RX MEDLINE=94357216; PubMed=8076638;
 RA Watanabe Y., Barbashov S.F., Komatsu S., Hemmings A.M., Miyagi M.,
 RA Tsunashima S., Hirano H.;
 RT "A peptide that stimulates phosphorylation of the plant insulin-
 RT binding protein. Isolation, primary structure and cDNA cloning."
 RL Eur. J. Biochem. 224:167-172(1994).
 RN [2]

RP SEQUENCE FROM N.A.
 RA STRAIN-cv. Miyagishihrome;
 RA Tan J.Z., Lou C.F., Hirano H.;
 RT "Analysis of leginsulin gene in soybean cultivar (glycine max) and
 RT wild species (glycine soja)."
 RL Chin. J. Appl. Environ. Biol. 5:259-263(1999).
 RN [3]
 RP REVISION TO 64.
 RC STRAIN-cv. Miyagishihrome;
 RA Hirano H.;
 RL Submitted (JUN-2001) to the SWISS-PROT data bank.
 CC -1- FUNCTION: LEGINSULIN BINDS TO BASIC 7S GLOBULIN (BG) AND
 CC STIMULATES ITS PHOSPHORYLATION ACTIVITY. INVOLVED IN THE SIGNAL
 CC TRANSDUCTION SYSTEM TO REGULATE THE GROWTH AND DIFFERENTIATION AS
 CC A HORMONE PEPTIDE.
 CC -1- PTM: THREE DISULFIDE BONDS ARE PROBABLY PRESENT IN LEGINSULIN.
 CC -1- PTM: THE C-TERMINAL GLYCINE MAY BE REMOVED FROM LEGINSULIN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: D17396; BAA04219.1; -
 KW Seed storage protein; Albumin; Signal.
 FT SIGNAL 1 19
 FT 19
 FT CHAIN 20 56
 FT 57 64
 FT PROPEP 65 116
 FT 117 119
 FT 119 AA; 13046 MW; A054491D7BE1AA70 CRC64;

Query Match 16.6%; Score 26; DB 1; Length 119;
 Best Local Similarity 30.8%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29
 DB 14 PTKIEADDCGAC 26

RESULT 4

Y816_DROME STANDARD; PRT; 355 AA.
 ID Y816_DROME
 AC 09VAF0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein CG7816.
 GN CG7816.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 NC NCBL_txid=7227;
 RX MEDLINE-20196006; PubMed-10731132;
 RC STRAIN-Berkeley;
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
 RA Wen K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
 RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.K., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glogok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwu C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merklow G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Stryckas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 CC Science 287:2185-2195(2000).
 CC 1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC 1- SIMILARITY: BELONGS TO THE KIF4/CATSPF FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AE003771; AAF5660.1; -
 DR Flybase: FBgn0039714; CG816.
 DR InterPro: IPR003689; Zn_tntrptl.zip.
 DR Pfam: PF02535; Zip; 1.
 KM Hypothetical protein; Transmembrane; Glycoprotein.
 FT TRANSMEM 37 57 POTENTIAL.
 FT TRANSME 79 99 POTENTIAL.

FT TRANSMEM 118 138 POTENTIAL.
 FT TRANSMEM 273 293 POTENTIAL.
 FT TRANSMEM 301 321 POTENTIAL.
 FT CAROHD 4 4 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CAROHD 218 218 N-LINKED (GLCNAc...) (POTENTIAL).
 SQ SEQUENCE 355 AA; 38870 MW; 01527C0390741F8B CRC64;
 Query Match 16.6%; Score 26; DB 1; Length 355;
 Best Local Similarity 30.8%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 17 PXXXXXXCXKC 29
 DB 165 PEGTSESCGAC 177
 RESULT 5
 ID BMP3_RAT STANDARD; PRT; 468 AA.
 AC BMP3_RAT
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bone morphogenetic protein 3 precursor (BMP-3).
 GN BMP3 OR BMP-3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCBL_txid=10116;
 RX MEDLINE-95186061; PubMed-7880444;
 RC STRAIN-Sprague-Dawley; TISSUE-Calvaria;
 RA Takeo M., Hino J., Kangawa K., Matsuo H.;
 RL Submitted (Aug-1995) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 109-468 FROM N.A.
 RC TISSUE-Calvaria;
 RX MEDLINE-95186061; PubMed-7880444;
 RA Chen D., Feng J.Q., Feng M., Harris M.A., Mahy P., Mundy G.R.,
 RA Harris S.E.;
 RT "Sequence and expression of bone morphogenetic protein 3 mRNA in
 RT prolonged cultures of fetal rat calvarial osteoblasts and in rat
 RT prostate adenocarcinoma PA III cells."
 RT DNA Cell Biol. 14:235-239(1995).
 CC 1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
 CC 1- SUBUNIT: HOMODIMER: DISULFIDE-LINKED (BY SIMILARITY).
 CC 1- TISSUE SPECIFICITY: HIGH LEVELS IN TRACHEA, SPLEEN, SMALL
 CC INTESTINE, AND OVARY, AND AT LOW LEVELS IN CEREBELLUM, COSTA AND
 CC BONE MARROW.
 CC 1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: D63860; BA09922.1; -
 DR EMBL: S77492; AAB3725.1; -
 DR HSSP: P12643; 3BMP.
 DR InterPro: IPR002400; GF_cysknob.
 DR InterPro: IPR001839; TGFb.
 DR Pfam: PF00019; TGF-beta; 1.
 DR PRINTS: PR00438; GFCTSKNOT.
 DR ProDom: PDD00357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 KW Signal: Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 FT SIGNAL 1 22 POTENTIAL.
 FT PROPEP 23 358 POTENTIAL.
 FT CHAIN 359 468 BONE MORPHOGENETIC PROTEIN 3.

FT DISULFID 366 433 BY SIMILARITY.
 FT DISULFID 395 465 BY SIMILARITY.
 FT DISULFID 399 467 BY SIMILARITY.
 FT DISULFID 432 432 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 468 AA; 52675 MW; 05315D4954DC3C64;

Query Match 16.6%; Score 26; DB 1; Length 468;
 Best Local Similarity 30.8%; Pred. No. 5.3e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29
 DB 387 PKSFAYCSCGAC 399

RESULT 6
 BNP3_HUMAN
 ID BNP3_HUMAN STANDARD; PRT; 472 AA.
 AC P12645; 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bone morphogenetic protein 3 precursor (BMP-3) (osteogenin) (BMP-3A).
 GN BMP3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=89072730; PubMed=3201241;
 RA Wozney J.M., Rosen V., Celeste A.J., Mitscock L.M., Whitters M.J.,
 RA Kriz R.W., Hewick R.M., Wang E.A.;
 RT "Novel regulators of bone formation: molecular clones and
 RT activities.";
 RL Science 242:1528-1534(1988).
 CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LUNG, OVARY AND SMALL INTESTINE.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: M22491; AAA51836.1; -
 CC PIR: D37278; D37278.
 DR HSSP: P12643; 3BMP.
 DR Genew: HGNC:1070; BMP3.
 DR MIM: 112263;
 DR InterPro: IPR002400; GF_cysknot.
 DR InterPro: IPR001839; TGFb.
 DR Pfam: PF00019; TGF-beta.1.
 DR PRINTS: PR00438; GRCYSKNOT.
 DR Prodom: PD000357; TGFb.1.
 DR SMART: SM00204; TGFb.1.
 DR PROSITE: PS00250; TGF_BETA.1; 1.
 KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 362 POTENTIAL.
 FT CHAIN 363 472 BONE MORPHOGENETIC PROTEIN 3.
 FT DISULFID 370 437 BY SIMILARITY.
 FT DISULFID 399 469 BY SIMILARITY.
 FT DISULFID 403 471 BY SIMILARITY.

FT DISULFID 436 436 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 472 AA; 53406 MW; 95C3B7BD5C9D596F CRC64;

Query Match 16.6%; Score 26; DB 1; Length 472;
 Best Local Similarity 30.8%; Pred. No. 5.4e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29
 DB 391 PKSFAYCSCGAC 403

RESULT 7
 BMB3_MOUSE
 ID BMB3_MOUSE STANDARD; PRT; 476 AA.
 AC P9737;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bone morphogenetic protein 3b precursor (BMP-3b)
 DE (Growth/differentiation factor 10) (GDF-10).
 GN GDF10 OR BMP3B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC STRAIN=CD-1; TISSUE=Uterus;
 RX MEDLINE=96115614; PubMed=8679252;
 RA Cunningham N.S., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RA Reddi A.H., Lee S.-J.;
 RT "Growth/differentiation factor-10: a new member of the transforming
 RT growth factor-beta superfamily related to bone morphogenetic
 RT protein-3.";
 RL Growth Factors 12:99-109(1995).
 CC -1- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: Expressed in uterus, adipose tissue, brain and
 CC bone, and to a lesser extent in liver and spleen.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: S82648; AAB46753.1; -
 CC HSSP: P12643; 3BMP.
 DR MGD: MGI:95684; Gdf10.
 DR InterPro: IPR001839; TGFb.
 DR Pfam: PF00019; TGF-beta.1.
 DR Prodom: PD000357; TGFb.1.
 DR SMART: SM00204; TGFb.1.
 DR PROSITE: PS00250; TGF_BETA.1; 1.
 KW Signal; Growth factor; Cytokine; glycoprotein.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 366 POTENTIAL.
 FT CHAIN 367 476 BONE MORPHOGENETIC PROTEIN 3B.
 FT DISULFID 374 441 BY SIMILARITY.
 FT DISULFID 403 473 BY SIMILARITY.
 FT DISULFID 407 475 BY SIMILARITY.
 FT DISULFID 440 440 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 467 467 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 476 AA; 52490 MW; 15D4CB86540FE82 CRC64;

Query Match 16.6%; Score 26; DB 1; Length 476;
Best Local Similarity 30.8%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXKXC 29
DB 395 PKSFDAVYCAGAC 407

RESULT 8
BM3B_RAT STANDARD; PRT; 476 AA.

ID BM3B_RAT
AC P55108;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bone morphogenetic protein 3b precursor (BMP-3b)
DE (Growth/differentiation factor 10) (GDF-10) (Bone inducing protein)
DE (BIP).
GN GDF10 OR BMP3B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-Sprague-Dawley; TISSUE=Femur;
RX MEDLINE=96193707; PubMed=8605043;
RA Takao M., Hino J., Takeshita N., Konno Y., Nishizawa T.,
RA Matsuo H., Kangawa K.;
RT Identification of rat bone morphogenetic protein-3b (BMP-3b), a new
RT member of BMP-3.";
RT Biochem. Biophys. Res. Commun. 219:656-662(1996).
CC -1- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL).
CC -1- TISSUE SPECIFICITY: COSTA, COSTICARTILAGE, FEMUR, CALVARIA,
CC TRACHEA, AORTA AND BRAIN. PREDOMINANTLY IN THE CEREBELLUM.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC
CC
CC EMBL: D49494; BAA08454.1; -.
DR HSSP: P12643; 3BMP.
DR InterPro: IPR001839; TGFb.
DR Pfam: PF00019; TGF-beta; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
KW Signal; Growth factor; Cytokine; Glycoprotein.
FT SIGNAL 1
FT PROPEP 30 366
FT CHAIN 367 476
FT DISULFID 374 441
FT DISULFID 403 473
FT DISULFID 407 475
FT DISULFID 440 440
FT CARBOHYD 114 114
FT CARBOHYD 152 152
FT CARBOHYD 277 277
FT CARBOHYD 467 467
SQ SEQUENCE 476 AA; 52960 MW; 873F4D4150C625EE CRC64;

Query Match 16.6%; Score 26; DB 1; Length 476;
Best Local Similarity 30.8%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXKXC 29
DB 395 PKSFDAVYCAGAC 407

RESULT 9
BM3B_HUMAN STANDARD; PRT; 478 AA.

ID BM3B_HUMAN
AC P55107; G9UCX6;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bone morphogenetic protein 3b precursor (BMP-3b)
DE (Growth/differentiation factor 10) (GDF-10) (Bone inducing protein)
DE (BIP).
GN GDF10 OR BMP3B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Femur;
RX MEDLINE=96264636; PubMed=8670277;
RA Hino J., Takao M., Takeshita N., Konno Y., Nishizawa T.,
RA Matsuo H., Kangawa K.;
RT cDNA cloning and genomic structure of human bone morphogenetic
RT protein-3b (BMP-3b)."
RT Biochem. Biophys. Res. Commun. 223:304-310(1996).
RN [2]
RP SEQUENCE OF 360-478 FROM N.A.
RC TISSUE=uterus;
RX MEDLINE=96115614; PubMed=8679252;
RA Cunningham N.S., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RA Reddi A.H., Lee S.J.;
RT "Growth/differentiation factor-10: a new member of the transforming
RT growth factor-beta superfamily related to bone morphogenetic protein-
RT 3.";
RT Growth Factors 12:99-109(1995).
CC -1- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL).
CC -1- TISSUE SPECIFICITY: FEMUR, BRAIN, LUNG, SKELETAL MUSCLE, PANCREAS
CC AND TESTIS.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC
CC
CC EMBL: D49493; BAA08453.1; -.
DR HSSP: P12643; 3BMP.
DR InterPro: IPR001839; TGFb.
DR Pfam: PF00019; TGF-beta; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
KW Signal; Growth factor; Cytokine; Glycoprotein.
FT SIGNAL 1
FT PROPEP 34 368
FT CHAIN 369 478
FT DISULFID 376 443
FT DISULFID 405 475
FT DISULFID 409 477
FT DISULFID 442 442
FT CARBOHYD 118 118
FT CARBOHYD 156 156
SQ SEQUENCE 478 AA; 52960 MW; 873F4D4150C625EE CRC64;

Query Match 16.6%; Score 26; DB 1; Length 476;
Best Local Similarity 30.8%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 469 469 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 478 AA: 53121 MW: 80AE0FA4C50B23A9 CRC64;
 Query Match 16.6%; Score 26; DB 1; Length 478;
 Best Local Similarity 30.8%; Pred. No. 5.4e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 OY 17 PXXXXXXCXGXC 29
 DB 397 PKSFAYCAGAC 409
 RESULT 10
 TGF2_BOVIN STANDARD; PRT; 112 AA.
 AC P21214;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transforming growth factor beta 2 (TGF-beta 2) (Milk growth factor)
 DE (MGF).
 GN TGFb2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxId-9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Milk;
 RX MEDLINE-92189724; PubMed-1799413;
 RA Jin Y., Cox D.A., Knecht R., Raschdorf F., Cerletti N.;
 RT "Separation, purification, and sequence identification of TGF-beta 1
 and TGF-beta 2 from bovine milk."
 RL J. Biol. Chem. 10:565-575(1991).
 RN [2]
 RP SEQUENCE OF 1-30.
 RC TISSUE-Bone;
 RX MEDLINE-87137406; PubMed-3469199;
 RA Seyedin S.M., Segarini P.R., Rosen D.M., Thompson A.V., Bentz H.,
 RA Graycar J.;
 RT "Cartilage-inducing factor-B is a unique protein structurally and
 RT functionally related to transforming growth factor-beta."
 RL J. Biol. Chem. 262:1946-1949(1987).
 RN [3]
 RP SEQUENCE OF 1-19.
 RC TISSUE-Milk;
 RX MEDLINE-91224126; PubMed-2026157;
 RA Cox D.A., David A., Buert R.R.;
 RT "Isolation and characterization of milk growth factor, a
 RT transforming-growth-factor-beta 2-related polypeptide, from bovine
 RT milk."
 RL Eur. J. Biochem. 197:353-358(1991).
 RN [4]
 RP SUBUNITS.
 RC TISSUE-Bone;
 RX MEDLINE-92129307; PubMed-1739336;
 RA Ogawa Y., Schmidt D.K., Dasch J.R., Chang R.J., Glaser C.B.;
 RT "Purification and characterization of transforming growth factor-beta
 RT 2.3 and -beta 1.2 heterodimers from bovine bone."
 RL J. Biol. Chem. 267:2325-2328(1992).
 CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
 CC DEPENDENT T-CELL GROWTH.
 CC -1- SUBUNIT: HOMODIMER: DISULFIDE-LINKED. HETERODIMERS OF TGF-BETA 1/2
 CC AND OF TGF-BETA 2/3 HAVE BEEN FOUND IN BONE.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR PIR: S15389; S15389.
 DR HSSP: P08112; 2TGI.
 DR InterPro: IPR002400; GF_cysknot.
 DR InterPro: IPR001839; TGFb.
 DR Pfam: PF00019; TGF-Delta; 1.

DR PRINTS: PR00438; GFCYSKNOT.
 DR PRODOM: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF-BETA 1; 1.
 KW Growth factor; Mitogen; Milk.
 FT DISULFID 7 16 BY SIMILARITY.
 FT DISULFID 15 78 BY SIMILARITY.
 FT DISULFID 44 109 BY SIMILARITY.
 FT DISULFID 48 111 BY SIMILARITY.
 FT DISULFID 77 77 INTERCHAIN (BY SIMILARITY).
 SQ SEQUENCE 112 AA: 12719 MW: 5142C7432C4BEC1C CRC64;
 Query Match 15.9%; Score 25; DB 1; Length 112;
 Best Local Similarity 30.8%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 OY 17 PXXXXXXCXGXC 29
 DB 36 PKGYNAFCAGAC 48
 RESULT 11
 BM8B_MOUSE STANDARD; PRT; 399 AA.
 ID BM8B_MOUSE
 AC P51105;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bone morphogenetic protein 8B precursor (BMP-8B).
 DE BMP8B.
 CN Mus musculus (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxId-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ICR; TISSUE-Placenta;
 RX MEDLINE-97000308; PubMed-8843393;
 RA Zhao G.Q., Hogan B.L.;
 RT "Evidence that mouse Bmp8a (Op2) and Bmp8b are duplicated genes that
 RT play a role in spermatogenesis and placental development."
 RL Mech. Dev. 57:159-168(1996).
 CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE
 CC OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF
 CC EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION
 CC AND BONE HOMEOSTASIS (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER: DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@sdb-sdb.ch).
 CC -----
 DR EMBL: U39545; AAB17573.1; -.
 DR HSSP: P18075; 1BMP.
 DR MCD: MG1107335; Bmp8b.
 DR InterPro: IPR002400; GF_cysknot.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR001111; TGFb.N.
 DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGFb_propeptide; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR PRODOM: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF-BETA 1; 1.
 KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 FT SIGNAL 1 19 POTENTIAL.
 FT PROPEP 20 260

FT CHAIN 261 399 BONE MORPHOGENETIC PROTEIN 8B.
FT DISULFID 364 396 BY SIMILARITY.
FT DISULFID 327 396 BY SIMILARITY.
FT DISULFID 331 398 BY SIMILARITY.
FT DISULFID 363 363 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 399 AA; 44752 MW; EFA0B78C7EC4839 CRC64;
Query Match 15.9%; Score 25; DB 1; Length 399;
Best Local Similarity 30.8%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 17 PXXXXXXCXKXC 29
DB 319 PGYSAYCAGEC 331
RESULT 12
TGF2_CHICK STANDARD; PRT; 412 AA.
AC P30371;
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 2 precursor (TGF-beta 2).
GN TGFb2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Blood;
RX MEDLINE=92075163; PubMed=1683775;
RA Burt D.W., Paton I.R.;
RT "Molecular cloning and primary structure of the chicken transforming
growth factor-beta 2 gene."
RL DNA Cell Biol. 10:723-734(1991).
CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
DEPENDENT T-CELL GROWTH.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
DR EMBL: X58071; CAA1101.1;
DR EMBL: X59082; CAA1101.1; JOINED.
DR EMBL: X59081; CAA1101.1; JOINED.
DR EMBL: X59080; CAA1101.1; JOINED.
DR PIR: A39489; A39489.
DR HSSP: P08112; 2TGT.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR003911; TGF_TGFB.
DR InterPro: IPR001839; TGFB.
DR InterPro: IPR001111; TGFB.N.
DR Pfam: PF000019; TGF-beta; 1.
DR Pfam: PF00688; TGFB_propeptide; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR01423; TGFbeta.
DR PRODOM: PD000357; TGFB.N.
DR SMART: SM00204; TGFB; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 20 POTENTIAL.

FT PROPEP 21 300 TRANSFORMING GROWTH FACTOR BETA 2.
FT CHAIN 301 412 BY SIMILARITY.
FT DISULFID 307 316 BY SIMILARITY.
FT DISULFID 315 378 BY SIMILARITY.
FT DISULFID 344 409 BY SIMILARITY.
FT DISULFID 348 411 BY SIMILARITY.
FT DISULFID 377 377 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 412 AA; 47606 MW; 93E759BF1BD958DC CRC64;
Query Match 15.9%; Score 25; DB 1; Length 412;
Best Local Similarity 30.8%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 17 PXXXXXXCXKXC 29
DB 336 PRGYHANFCAGAC 348
RESULT 13
TGF2_XENLA STANDARD; PRT; 413 AA.
ID TGF2_XENLA
AC P17247;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 2 precursor (TGF-beta 2).
GN TGFb2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90245678; PubMed=2336403;
RA Rebert M.L., Bhatia-Dey N., David I.B.;
RT "The sequence of TGF-beta 2 from Xenopus laevis."
RL Nucleic Acids Res. 18:2185-2185(1990).
CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
DEPENDENT T-CELL GROWTH.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
DR EMBL: X51817; CAA36116.1;
DR EMBL: X51817; CAA36117.1; ALT_INT.
DR PIR: S09510; S09510.
DR HSSP: P08112; 2TGT.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR003911; TGF_TGFB.
DR InterPro: IPR001839; TGFB.
DR InterPro: IPR001111; TGFB.N.
DR Pfam: PF000019; TGF-beta; 1.
DR Pfam: PF00688; TGFB_propeptide; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR01423; TGFbeta.
DR PRODOM: PD000357; TGFB.N.
DR SMART: SM00204; TGFB; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Signal; Mitogen; Glycoprotein; Growth factor.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 301

FT CHAIN 302 413 TRANSFORMING GROWTH FACTOR BETA 2.
 FT DISULFID 308 317 BY SIMILARITY.
 FT DISULFID 316 379 BY SIMILARITY.
 FT DISULFID 345 410 BY SIMILARITY.
 FT DISULFID 349 412 BY SIMILARITY.
 FT DISULFID 378 378 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 72 72 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAc. . .) (POTENTIAL).
 SQ SEQUENCE 413 AA; 47639 MW; 6127715838734010 CRC64;
 Query Match 15.9%; Score 25; DB 1; Length 413;
 Best Local Similarity 30.8%; Pred. No. 7.1e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Oy 17 PXXXXXXCXGXC 29
 Db 337 PKGYNANFCGAC 349
 RESULT 14
 TGF2_HUMAN STANDARD: PRF: 414 AA.
 AC P08112: Q15579; Q15581;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transforming growth factor beta 2 precursor (TGF-beta 2)
 DE (Gliblastoma-derived T-cell suppressor factor) (G-TSF) (BSC-1 cell
 DE growth inhibitor) (Polyergin) (Cetermin).
 GN TGF2.
 OS Homo sapiens (Human), and
 OS Cercopithecus aethiops (Green monkey) (Griwet).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606, 9534;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC SPECIES-Human;
 RX MEDLINE=88116555; PubMed=3322813;
 RA de Martin R., Haendler B., Hofer-Warbinek R., Gaugitsch H., Wranz M.,
 RA Schluessener H., Siefert J.M., Bodmer S., Fontana A., Hofer E.,
 RT "Complementary DNA for human gliblastoma-derived T cell suppressor
 RT factor," a novel member of the transforming growth factor-beta gene
 RT family.";
 RL EMBO J. 6:3673-3677(1987).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM B).
 RC SPECIES-Human;
 RX MEDLINE=88166349; PubMed=3162414;
 RA Madisen L., Webb N.R., Rose T.M., Marguardt H., Ikeda T.,
 RA Twardzik D.R., Seyedin S., Purchio A.F.;
 RT "Transforming growth factor-beta 2: cDNA cloning and sequence
 RT analysis";
 RL DNA 7:1-8(1988).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
 RC SPECIES-Human;
 RX MEDLINE=89090808; PubMed=2850146;
 RA Webb N.R., Madisen L., Rose T.M., Purchio A.F.;
 RT "Structural and sequence analysis of TGF-beta 2 cDNA clones predicts
 RT two different precursor proteins produced by alternative mRNA
 RT splicing";
 RL DNA 7:493-497(1988).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC SPECIES-C.aethiops;
 RX MEDLINE=88124824; PubMed=3277172;
 RA Hanks S., Armour R., Baldwin J.H., Maldonado F., Spleess J.,
 RA Holley R.W.;
 RT "Amino acid sequence of the BSC-1 cell growth inhibitor (polyergin)
 RT deduced from the nucleotide sequence of the cDNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:79-82(1988).

RN [5]
 RP SEQUENCE OF 1-115 FROM N.A.
 RC SPECIES-Human; TISUE=Lung;
 RX MEDLINE=92110032; PubMed=1764261;
 RA Noma T., Glick A.B., Geiser A.C., O'Reilly M.A., Miller J.,
 RA Roberts A.B., Sporn M.B.;
 RT "Molecular cloning and structure of the human transforming growth
 RT factor-beta 2 gene promoter.";
 RN Growth Factors 4:247-255(1991).
 RN [6]
 RP SEQUENCE OF 303-414.
 RC SPECIES-Human;
 RX MEDLINE=87308213; PubMed=3476488;
 RA Marguardt H., Liobin M.N., Ikeda T.;
 RT "Complete amino acid sequence of human transforming growth factor
 RT type beta 2.";
 RN J. Biol. Chem. 262:12127-12131(1987).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RX MEDLINE=92335881; PubMed=1631557;
 RA Daopin S., Pletz K.A., Ogawa Y., Davies D.R.;
 RT "Crystal structure of transforming growth factor-beta 2: an unusual
 RT fold for the superfamily.";
 RN Science 257:369-373(1992).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=92350287; PubMed=1641027;
 RA Schlunegger M.P., Gruetter M.G.;
 RT "An unusual feature revealed by the crystal structure at 2.2-A
 RT resolution of human transforming growth factor-beta 2.";
 RN Nature 358:430-434(1992).
 RN [9]
 RP VARIANT HIS-91.
 RX MEDLINE=21419167; PubMed=11528528;
 RA Alansari A., Hajjari A.H., Bayat A., Eyre S., Carthy D., Ollier W.E.;
 RT "Two novel polymorphisms in the human transforming growth factor beta
 RT 2 gene.";
 RL Genes Immun. 2:295-296(2001).
 CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
 CC DEPENDENT T-CELL GROWTH.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING. ISOFORM B IS ENCODED BY A MINOR
 CC 5.1 KB MRNA SPECIES PRESENT IN HUMAN AND SIMIAN CELLS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 CC -----
 CC EMBL: Y00083; CAA68279.1; -;
 CC EMBL: M19154; AAA50404.1; -;
 CC EMBL: M19154; AAA50405.1; ALT_SEQ.
 CC EMBL: J03585; AAA33558.1; -;
 CC EMBL: M87843; AAA61162.1; -;
 CC PIR: S06216; S06216.
 CC PIR: A29478; A29478.
 CC PIR: A29798; A29798.
 CC PIR: A34005; A34005.
 CC PDB: 1TEG; 3I-OCT-93.
 CC PDB: 2TGT; 3I-JAN-94.
 CC Genew; HGNC:11768; TGF2.
 CC MIM: 190220; -;
 CC InterPro: IPR002400; GF_cysknob.
 CC InterPro: IPR003911; TGF_TGFB.
 CC InterPro: IPR001839; TGFB.
 CC InterPro: IPR001111; TGFB_N.
 CC Pfam: PF00019; TGF-beta; 1.

DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PRINTS; PR01423; TGFbeta.
 DR PRODOM; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR Growth factor; Mitogen; Glycoprotein; Signal; Alternative splicing;
 RW 3D-structure.
 FT SIGNAL 1 19
 FT PROPEP 20 302
 FT CHAIN 303 414
 FT DISULFID 309 318
 FT DISULFID 317 380
 FT DISULFID 346 411
 FT DISULFID 350 413
 FT DISULFID 379 379
 FT CARBOHYD 72 72
 FT CARBOHYD 140 140
 FT CARBOHYD 241 241
 FT VARSPLIC 116 116
 FT VARIANT 91 91
 FT CONFLICT 32 32
 FT HELIX 306 309
 FT TURN 310 311
 FT STRAND 316 316
 FT STRAND 318 320
 FT STRAND 323 325
 FT HELIX 326 330
 FT TURN 333 334
 FT STRAND 335 337
 FT STRAND 340 342
 FT STRAND 345 347
 FT STRAND 349 349
 FT TURN 352 353
 FT STRAND 356 356
 FT HELIX 359 370
 FT HELIX 372 374
 FT STRAND 380 382
 FT STRAND 385 394
 FT TURN 395 396
 FT STRAND 397 408
 FT STRAND 411 413
 SQ SEQUENCE 414 AA; 47747 MW; 7D9D569E0FA07D0 CRC64;
 Query Match 15.98; Score 25; DB 1; Length 414;
 Best Local Similarity 30.88; Pred. No. 7.1e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 OY 17 PXXXXXXXXXXGXC 29
 DB 338 PKGYNANFCAGAC 350
 RESULT 15
 TGF2_MOUSE
 ID TGF2_MOUSE STANDARD; PRT; 414 AA.
 AC P27090;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transforming growth factor beta 2 precursor (TGF-beta 2).
 GN TGFb2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90014832; PubMed=2797004;
 RA Miller D.A., Lee A., Pelton R.W., Chen E.Y., Moses H.L.,
 Derynck R.;

RT "Murine transforming growth factor-beta 2 cDNA sequence and
 expression in adult tissues and embryos."
 RL Mol. Endocrinol. 3:1108-1114(1989).
 CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
 CC DEPENDENT T-CELL GROWTH.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-slb.ch/announce/>
 CC or send an email to license@isb-slb.ch).
 CC -----
 DR EMBL; X57413; CAA00672.1; -.
 DR PIR; A40148; WFM5B2.
 DR HSSP; P08112; 2TGI.
 DR MGD; MGI:98726; TgfB2.
 DR InterPro; IPR002400; GF_cysknott.
 DR InterPro; IPR003911; TGF_TGFb.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PRINTS; PR01423; TGFbeta.
 DR PRODOM; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR Growth factor; Mitogen; Glycoprotein; Signal.
 KW Growth factor; Mitogen; Glycoprotein; Signal.
 FT SIGNAL 1 19
 FT PROPEP 20 302
 FT CHAIN 303 414
 FT DISULFID 309 318
 FT DISULFID 317 380
 FT DISULFID 346 411
 FT DISULFID 350 413
 FT DISULFID 379 379
 FT CARBOHYD 72 72
 FT CARBOHYD 140 140
 FT CARBOHYD 241 241
 SQ SEQUENCE 414 AA; 47601 MW; 449BC6FA22087FB6 CRC64;
 Query Match 15.98; Score 25; DB 1; Length 414;
 Best Local Similarity 30.88; Pred. No. 7.1e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 OY 17 PXXXXXXXXXXGXC 29
 DB 338 PKGYNANFCAGAC 350

Search completed: March 27, 2003, 11:00:10
 Job time : 26 secs

SO SEQUENCE 102 AA; 9749 MW; 8BFE5ABD6AE78857 CRC64;
 Query Match 17.2%; Score 27; DB 11; Length 102;
 Best Local Similarity 30.8%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXKXGXC 29
 DB 27 PASSSSSCGGGC 39

RESULT 2
 OY9754 PRELIMINARY; PRT; 549 AA.
 AC OY9754;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE Siderophore biosynthesis repressor SREA.
 GN SREA.
 OS Emeritella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emeritella.
 OX NCBI_TaxID=5072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99143116; PubMed=9988696;
 RA Haas H., Zadra I., Scofield G., Angermayr K.;
 RT "The Aspergillus nidulans GATA factor SREA is involved in regulation
 of siderophore biosynthesis and control of iron uptake.";
 RL J. Biol. Chem. 274:4613-4619(1999).
 DR EMBL: AF095898; AAD25328.1;
 DR HSP; P17679; IGNF.
 DR InterPro: IPR000679; Znf_GATA.
 DR Pfam: PF00320; GATA. 2.
 DR PRINTS: PR00619; GATAZNFINGER.
 DR SMART: SM00401; ZNF_GATA. 2.
 DR PROSITE: PS00344; GATA_ZN_FINGER. 1; 2.
 DR PROSITE: PS00114; GATA_ZN_FINGER. 2;
 SO SEQUENCE 549 AA; 58842 MW; 539DC02AEFD62E3 CRC64;

Query Match 17.2%; Score 27; DB 3; Length 549;
 Best Local Similarity 30.8%; Pred. No. 8.2e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXKXGXC 29
 DB 168 PAVTSGEGCTGSC 180

RESULT 3
 OY080540 PRELIMINARY; PRT; 967 AA.
 AC OY080540;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE FlA39.26 protein.
 GN FlA39.26.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Federapfel N.A., Palm C.J., Conway A.B., Kurtz D.B., Conway A.R.,
 Au M., Araujo R., Buehler E., Dewar K., Feng J., Kim C., Li Y.,
 Oja O., Osborne B.J., Shin P., Sun H., Tortum M., Vysotskaia V.S.,
 Yu G., Ecker J., Theologis A., Davis R.W.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL: AC003970; AAC33218.1; -.
 DR HSP; P24941; IHCL.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR ProDom: PD000001; Euk_pkinase.1.
 DR SMART: SM00220; S_TKc. 1.
 DR PROSITE: PS0107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR AMP-binding; Serine/threonine-protein kinase; Transferase.
 SO SEQUENCE 967 AA; 108177 MW; 6EB7F336C51289 CRC64;

Query Match 17.2%; Score 27; DB 10; Length 967;
 Best Local Similarity 30.8%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXKXGXC 29
 DB 726 P0ETSTRGSGAC 738

RESULT 4
 OY042306 PRELIMINARY; PRT; 87 AA.
 AC OY042306;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Transforming growth factor beta (Fragment).
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OX NCBI_TaxID=7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MACROPHAGE;
 RA Daniels G.D., Belosevic M., Secombes C.J.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
 RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL: A001040; CAA04494.1; -.
 DR HSP; P01137; IKLA.
 DR InterPro: IPR001839; TGF.
 DR Pfam: PF00019; TGF-beta. 1.
 DR ProDom: PD000357; TGF. 1.
 DR SMART: SM00204; TGF. 1.
 DR PROSITE: PS00250; TGF_BETA.1; 1.
 DR Growth factor; Mitogen; Glycoprotein.
 FT NON_TER 1
 FT CHAIN 1
 FT DISULFID <1 >87
 FT DISULFID 22 87
 FT DISULFID 55 87
 FT NON_TER 87 87
 SO SEQUENCE 87 AA; 10007 MW; 525465C4E8A70771 CRC64;

Query Match 16.6%; Score 26; DB 13; Length 87;
 Best Local Similarity 30.8%; Pred. No. 4.7e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXKXGXC 29
 DB 14 PGGYANYCTGSC 26

RESULT 5
 OY0924A9 PRELIMINARY; PRT; 230 AA.
 AC OY0924A9;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)

01-MAY-1999 (TREMblrel. 10, last sequence update)
 01-DEC-2001 (TREMblrel. 19, last annotation update)
 DE Tram protein.
 GN Shigella sonnei.
 OS Shigella Colib-P9.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Shigella.
 OX NCB1_TaxID=624;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-P9; Mizobuchi K.;
 RA "Organization and diversification of plasmid genomes: complete
 RT nucleotide sequence of the Colib-P9 genome."
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021078; BAA75159.1; -
 KW Plasmid.
 SQ SEQUENCE 230 AA; 25561 MW; FEE050B813F09FA1 CRC64;
 Query Match 16.6%; Score 26; DB 2; Length 230;
 Best Local Similarity 30.8%; Pred. No. 7.8e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

0Y 17 PXXXXXXCXGXC 29
 DB 38 PALIKALCTGTC 50

RESULT 6
 09R2H2 PRELIMINARY; PRT; 230 AA.
 AC 09R2H2;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
 DE Tram protein.
 GN TRAM.
 OS Salmonella typhimurium.
 OG Plasmid R64.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCB1_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DRD-11;
 RA Komano T., Narehara K., Yoshida T., Furuya N.;
 RT "The transfer region of IncII plasmid R64: similarities between R64
 RL tra genes and Legionella lcn/dot genes."
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DRD-11;
 RX MEDLINE=92011438; PubMed=1917882;
 RA Furuya N., Komano T.;
 RT "Determination of the nick site at oriT of IncII plasmid R64: global
 RL similarity of oriT structures of IncII and IncP plasmids."
 RL J. Bacteriol. 173:6612-6617(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DRD-11;
 RX MEDLINE=98053841; PubMed=9393692;
 RA Furuya N., Komano T.;
 RT "Mutational analysis of the R64 oriT region: requirement for precise
 RL location of the Nika-binding sequence."
 RL J. Bacteriol. 179:7291-7297(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DRD-11;
 RX MEDLINE=98268996; PubMed=9603870;
 RA Yoshida T., Furuya N., Ishikura M., Isobe T., Haino-Fukushima K.,
 OGawa T., Komano T.;
 RT "Purification and characterization of thin pill of IncII plasmids

Colib-P9 and R64: formation of pill-specific cell aggregates by type
 IV pill."
 RL J. Bacteriol. 180:2842-2848(1998).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DRD-11;
 RX MEDLINE=94132048; PubMed=8300611;
 RA Pansegrau W., Schröder W., Lanka E.;
 RT "Concerted action of three distinct domains in the DNA cleaving-
 RT joining reaction catalyzed by relaxase (Tral) of conjugative plasmid
 RP4."
 RL J. Biol. Chem. 269:2782-2789(1994).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DRD-11;
 RX MEDLINE=94485211; PubMed=8014987;
 RA Pansegrau W., Lanka E., Barth P.T., Figurski D.H., Guiney D.G.,
 HAas D., Helinski D.R., Schwab H., Stanisich V.A., Thomas C.M.;
 RT "Complete nucleotide sequence of Birmingham IncP-alpha plasmids:
 RT compilation and comparative analysis."
 RL J. Mol. Biol. 239:623-663(1994).
 DR EMBL; AB027308; BAA78001.1; -
 KW Plasmid.
 SQ SEQUENCE 230 AA; 25560 MW; F43394751D05AB90 CRC64;

Query Match 16.6%; Score 26; DB 2; Length 230;
 Best Local Similarity 30.8%; Pred. No. 7.8e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

0Y 17 PXXXXXXCXGXC 29
 DB 38 PALIKALCTGTC 50

RESULT 7
 09SDK7 PRELIMINARY; PRT; 240 AA.
 AC 09SDK7;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
 DE Hypothetical protein.
 GN Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoidae; Oryzae; Oryza.
 OX NCB1_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RL clone: P0705D01."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP000492; BAA84609.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 240 AA; 26333 MW; E67BC59CB18F9BD CRC64;
 Query Match 16.6%; Score 26; DB 10; Length 240;
 Best Local Similarity 30.8%; Pred. No. 8e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

0Y 17 PXXXXXXCXGXC 29
 DB 146 PAAAAAFGCGPC 158

RESULT 8
 09H7T3 PRELIMINARY; PRT; 257 AA.
 AC 09H7T3;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, last sequence update)

01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE CDNA FLJ14280 fis, clone PLACE1005584, weakly similar to trans-acting
 DE transcriptional protein ICP0.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RA TISSUE=PLACENTA;
 RA Isogat T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shitatori A., Sudo H.,
 RA Wagatsuma M., Hosokawa T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakami K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,
 RA Niimura K., Watanabe T.;
 RT "Genome sequence of the nematode C. elegans: A platform for
 RU submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK024342; BAB14892.1;
 SQ SEQUENCE 257 AA; 26269 MW; B914A57EA54DF418 CRC64;

Query Match 16.6%; Score 26; DB 4; Length 257;
 Best Local Similarity 30.8%; Pred. No. 8.3e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29
 DB 179 PLCTRTSCAGSC 191

RESULT 9
 ID 017764 PRELIMINARY; PRT; 278 AA.
 AC 017764;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 GN F01G10.6 protein.
 GN F01G10.6
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 RN [1]
 NCBI_TaxID=6239;
 RP SEQUENCE FROM N.A.
 RA Hemphry C.;
 RA Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 RU investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL: Z81055; CAB02894.1;
 SQ SEQUENCE 278 AA; 30945 MW; 9C5B0F9F3C88577A CRC64;

Query Match 16.6%; Score 26; DB 5; Length 278;
 Best Local Similarity 30.8%; Pred. No. 8.6e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29
 DB 59 PSMTFAESCSGPC 71

RESULT 10
 ID 018027 PRELIMINARY; PRT; 347 AA.
 AC 018027;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE T05E12.1 protein.
 GN T05E12.1
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 RN [1]
 NCBI_TaxID=6239;
 RP SEQUENCE FROM N.A.
 RA McMurray A.A.;
 RA Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 RU investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL: Z81585; CAB04681.1;
 DR InterPro: IPR003002; TrmChemol.
 DR Pfam: PF01461; Trm_4; 1.
 SQ SEQUENCE 347 AA; 39762 MW; B97BA2961988A85A CRC64;

Query Match 16.6%; Score 26; DB 5; Length 347;
 Best Local Similarity 30.8%; Pred. No. 9.6e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29
 DB 87 PLATTSRGFLC 99

RESULT 11
 ID 08R209 PRELIMINARY; PRT; 349 AA.
 AC 08R209;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 GN Hypothetical 39.1 kDa protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RA TISSUE=COLON;
 RA Strausberg R.;
 RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC022669; AAH22669.1;
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 349 AA; 39115 MW; D361C92578686F63 CRC64;

Query Match 16.6%; Score 26; DB 11; Length 349;
 Best Local Similarity 30.8%; Pred. No. 9.7e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29
 DB 268 PKSPDAYCAGAC 280

RESULT 12
 ID 09DFC6 PRELIMINARY; PRT; 366 AA.
 AC 09DFC6;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE TGF-beta family member lefty-A.
 OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20341055; PubMed=10882517;
 RA Brantford W.W., Essner J.J., Yost H.J.;
 RT "Regulation of gut and heart left-right asymmetry by context-dependent
 interactions between Xenopus lefty and BMP4 signaling.";
 RL Dev. Biol. 223:291-306(2000).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AF283562; AAC10034.1; -.
 DR HSSP; P18075; IBM.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Glycoprotein.
 SQ SEQUENCE 366 AA; 41434 MW; E65CEC306F4B5ED5 CRC64;
 Query Match 16.6%; Score 26; DB 13; Length 366;
 Best Local Similarity 30.8%; Pred. No. 9.9e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 OY 17 PXXXXXXCXGXC 29
 DB 293 PAGYNAFRCGSC 305
 RESULT 13
 O9D36 PRELIMINARY; PRT; 367 AA.
 AC O9D36;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Xantivin (Lefty-related factor Xatv).
 GN XANTIVIN.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11091069;
 RA Tanegashima K., Yokota C., Takahashi S., Asashima M.;
 RT "Expression cloning of Xantivin, a Xenopus lefty/antiyvin-related gene,
 involved in the regulation of activin signaling during mesoderm
 induction.";
 RL Mech. Dev. 99:3-14(2000).
 CC [2]
 RN SEQUENCE FROM N.A.
 RP Cheng A.M.S., Thisse B., Thisse C., Wright C.V.E.;
 RA "The lefty-related factor Xatv acts as a feedback inhibitor of nodal
 signaling in mesoderm induction and L-R axis development in Xenopus.";
 RT development 0-0-0(2000)
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AB038010; BAB12725.1; -.
 DR EMBL; AF209744; AAG35771.1; -.
 DR HSSP; P08112; 2TGI.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Glycoprotein.

SQ SEQUENCE 367 AA; 41504 MW; DEAA90275BC8574A CRC64;
 Query Match 16.6%; Score 26; DB 13; Length 367;
 Best Local Similarity 30.8%; Pred. No. 9.9e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 OY 17 PXXXXXXCXGXC 29
 DB 293 PAGYNAFRCGSC 305
 RESULT 14
 O9DFCS PRELIMINARY; PRT; 367 AA.
 AC O9DFCS;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE TGF-beta family member lefty-B.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20341055; PubMed=10882517;
 RA Brantford W.W., Essner J.J., Yost H.J.;
 RT "Regulation of gut and heart left-right asymmetry by context-dependent
 interactions between Xenopus lefty and BMP4 signaling.";
 RL Dev. Biol. 223:291-306(2000).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AF283563; AAC10035.1; -.
 DR HSSP; P08112; 2TGI.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Glycoprotein.
 SQ SEQUENCE 367 AA; 41604 MW; DBA7E85752B7FB3A CRC64;
 Query Match 16.6%; Score 26; DB 13; Length 367;
 Best Local Similarity 30.8%; Pred. No. 9.9e+02;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 OY 17 PXXXXXXCXGXC 29
 DB 293 PAGYNAFRCGSC 305
 RESULT 15
 O9PTQ2 PRELIMINARY; PRT; 376 AA.
 AC O9PTQ2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Transforming growth factor beta precursor.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yin Z., Kuang J.;
 RT "Molecular cloning of carp transforming growth factor beta 1.";
 RL submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
 RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.

CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC EMBL: AF136947; AAF22573.1; -.
 DR HSSP: P01137; IKLA.
 DR InterPro: IPR001839; TGF β .
 DR InterPro: IPR001111; TGF β _N.
 DR Pfam: PF00688; TGF β -propeptide; 1.
 DR ProDom: PD000357; TGF β ; 1.
 DR SMART: SM00204; TGF β ; 1.
 DR PROSITE: PS00250; TGF β _BETA_1; 1.
 KW Growth factor: Mitogen; Glycoprotein; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT PROPEP 23 264
 FT CHAIN 265 376 TRANSFORMING GROWTH FACTOR BETA.
 FT DISULFID 272 280 BY SIMILARITY.
 FT DISULFID 308 373 BY SIMILARITY.
 FT DISULFID 312 375 BY SIMILARITY.
 FT DISULFID 341 341 BY SIMILARITY.
 FT CARBOHYD 76 76 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SITE 230 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 376 AA; 43329 MM; 7F7FC4DA58B69681 CRC64; CELL ATTACHMENT SITE (POTENTIAL).
 Query Match 16.68; Score 26; DB 13; Length 376;
 Best Local Similarity 30.88; Pred. No. 1e+03;
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 17 PXXXXXXCXGXC 29
 DB 300 PSGYANCTGSC 312

Search completed: March 27, 2003, 11:01:43
 Job time : 87 secs